

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 104996

TO: Phillip Gambel Location: cm1/9e12

Art Unit: 1644

Friday, October 03, 2003

Case Serial Number: 09758173

From: Toby Port

Location: Biotech-Chem Library

CM1-6A04

Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Gambel,

Here are the results of your search.

Please feel free to contact me if you have any questions.

Toby Port

RUSH

09/758173



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Anderson, Darrell R.
WONKEY MONOCLONAL ANTIBODIES SPECIFIC
WEWTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: TO HARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
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MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: O7-JUN-1995
ATTONEY/AGENT INFORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REPERENCE/POCKET NUMBER: 31,030
REPERENCE/POCKET NUMBER: 35,030
REPERENCE/POCKET NUMBER: 35,030
REPERENCE/POCKET NUMBER: 35,030
REPERENCE/POCKET NUMBER: 35,030
RELERA: 703-836-620
TELEFRA: 703-836-620
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBOD
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SECUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                  US-00-488-376-17
US-08-634-223-17
US-08-634-400-17
US-08-634-400-17
US-08-70-057-17
US-09-335-6978-17
US-09-335-6978-17
US-09-740-002-17
US-09-740-002-17
US-08-26-098-11
US-08-26-098-11
US-08-286-740-3
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US-09-049-672A-21
PCT-US96-13152-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08487550 Patent No. 6113898 GENERAL INFORMATION:
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) LOCATION:

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                                                                                                                                                                                                                                       US-09-758-173-7
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US-08-157-101A-6
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US-08-149-68-3
US-09-023-715-2
US-09-023-715-0
US-09-023-19-0
US-08-034-340A-68
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                         version 5 - 2003 C
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Maximum Match 100%
Listing first 45 summaries
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Sequence 230, App
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Sequence 25, Appl
Sequence 27, Appl
Sequence 20, Appl
Sequence 20, Appl
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(without alignments)
12894.584 Million cell updates/sec
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2: 'cgn2_6/ptodata/2/pubpna/USO5_NUBM_PUB.seq:*
3: 'cgn2_6/ptodata/2/pubpna/USO6_NUBM_PUB.seq:*
4: 'cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
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6: 'cgn2_6/ptodata/2/pubpna/USO7_NUBM_PUB.seq:*
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8: 'cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: 'cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: 'cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: 'cgn2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
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3 US-10-124-905-7

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US-09-822-830A-572

US-09-822-299-230

2 US-09-825-299-230

2 US-09-825-108A-1

2 US-09-84B-832-1

2 US-09-84B-832-1

3 US-10-066-895-25

3 US-10-066-895-27

US-09-822-849A-111

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  GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
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17 1147.8 79.9 1392 14 US-10-150-475A-7 Sequence 7, Appli 18 1142.8 79.5 1538 9 US-09-822-849A-103 Sequence 103, Appli 1142.8 79.5 1534 10 US-09-822-830A-373 Sequence 103, Appli 20 1141.4 79.4 1315 10 US-09-822-698A-27 Sequence 27, Appli 21 1141.4 79.4 131.1 2 US-10-25-108A-15 Sequence 27, Appli 22 1138.6 79.2 1347 10 US-09-822-849A-114 Sequence 27, Appli 23 1138.6 79.2 1590 9 US-09-822-849A-114 Sequence 27, Appli 24 1138.6 79.2 1590 9 US-09-822-849A-114 Sequence 114, Appli 25 1133.4 78.9 1599 10 US-09-954-456-789 Sequence 114, Appli 26 1133.4 78.9 1599 10 US-09-954-456-789 Sequence 789, Appli 26 1133.4 78.9 1599 10 US-09-954-456-780 Sequence 1010, Appli 26 1133.4 78.9 1599 12 US-09-954-756-1604 Sequence 1010, Appli 27 1130.2 78.6 1449 10 US-09-970-703-1 Sequence 1.0 Appli 28 1130.2 78.6 1449 10 US-09-777-69-1 Sequence 1.0 Appli 29 1130.2 78.6 1449 14 US-10-290-703-1 Sequence 2, Appli 29 1130.2 78.6 1449 14 US-10-290-703-1 Sequence 2, Appli 37 1127.4 78.5 9209 11 US-09-921-12241 Sequence 3, Appli 37 1127.4 78.5 9209 11 US-09-91-696-928-2 Sequence 2, Appli 40 US-09-91-696-93-2 Sequence 2, Appli 41 US-10-290-926-93-2 Sequence 2, Appli 41 US-10-296-93-2 S
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RESCUET.

DESCRIPTION

SEQUENCE 7. Application US/09948429B

SEQUENCE 7. Application US/09948429B

SECULATION US/00177689AL

SEQUENCE 7. Application US/09948429B

PAPLICANT: Anderson, Darrell 8.

TITLE OF INVENTION: DARREX MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARAGEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS.

CORRESPONDENCE ADDRESS:

ADDRESSE: BURNS, DOANE, SWECKER & MATHIS

STREET: ADSOCRATION: STREET

CONFITE: VAR

COMPUTER: LARCAGUE FORM:

MINDER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC Compatible

COMPUTER: IBM PC Compatible

COMPUTER: TROPPY disk

COMPUTER: TROPPENTION DATA:

APPLICATION NUMBER: US/09/948,429B

FILING DATE:

APPLICATION NUMBER: US/09/948,250

FILING DATE:

APPLICATION NUMBER: US/09/948,550

FILING DATE:

APPLICATION NUMBER: 35,030

REFERENCE/COCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

NAME: TESKIO, ROBIO 1.

REGISTRATION NUMBER: 35,030

REFERENCE/COCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMENTER TOWN.
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"MONKET MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARKACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF
IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                      CICACCGIGGACAAGAGCAGGIGGCAGCAGGGGAACGICIICICAIGCICCGIGAIGCAI 1380
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                                        GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGCCGTGGAGGTGCATAATGCCAAGACA
CCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGAC
                          ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGACCACGAA
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APPLICATION NUMBER: US/10/124.807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/10124807
Publication No. US20030166207A1
GENERAL INPORMATION:
TITLE OF INVENTION: "MONNEY MONCE
TITLE OF INVENTION: TO HUMAN B7.1
TITLE OF INVENTION: TO HUMAN B7.1
TITLE OF INVENTION: IMMUNOSUPPRESA NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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100.0%;
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  INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1437 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 1437; Conservative
                                                                                                                                                     mat_peptide
                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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                                            TYPE: nucleic
STRANDEDNESS:
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LOCATION:
FEATURE:
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US-09-948-429B-7
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Compugen Ltd
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GenCore version
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		dР			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	QI	Description
н	2561	100.0	478	19	AAW63763	Macaque primatized
(7)	2561	100.0		23	AAU11644	Protein sequence o
m	2555	8.66		18	AAW01820	Primatised anti-h
4	2205	86.1		24	ABP58275	. Humanised 3D6 anti
Ŋ	2197	85.8		14	AAR42162	Anti-HIV-1 recomb
9	2184.5	85.3		20	AAY29458	Recombinant immun
7	2184.5	85.3		21	AAB30322	Humanised anti-IL
80	2184.5	85.3	452	21	AAY77766	Humanised anti-IL-
6	2184.5	85.3		24		Humanised Mouse a

WPI; 1998-286601/25. N-PSDB; AAV35487.

ALIGNMENTS

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Monoclonal antibody: Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Teall/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; I cell proliferation.
                                                                                            Macaque primatized 7B6 heavy chain protein.
                      AAW63763 standard; Protein; 478 AA
                                                                                                                                                                                                                                                                                                                                 Anderson DR, Brams P, Hanna N;
                                                                                                                                                                                                                                                                                    96US-0746361.
                                                                                                                                                                                                                                                             97WO-US19906
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                           (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                         Macaca fascicularis
                                                                                                                                                                                                              WO9819706-A1
                                                                                                                                                                                                                                                             29-OCT-1997;
                                                                                                                                                                                                                                                                                   08-NOV-1996;
                                                                     29-SEP-1998
                                                                                                                                                                                                                                      14-MAY-1998
                                             AAW63763;
RESULT 1
            AAW63763
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This sequence represents a primatized form of the antibody 7B6 heavy chain from macaque. This sequence is used in a method which studies new moncolonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such Mab's are specific immunosuppressants for treatment of diseases involving really entitle interactions, particularly autoimmune diseases, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. Mab's are optionally combined with other proteins or induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression.
                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and Inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                                                                                                         cells, e.g. graft rejection or tumours
                                                                                                                                                                  4b; 87pp; English
                                                                                                                                                                  Example 7; Fig
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478 AA; Sequence

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120
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                                                                                                                                                       GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
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                                                                   1 MGWSLILLFELVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                     Gaps
                                   ó
 100.0%; Score 2561; DB 19; Length 478; 100.0%; Pred. No. 4.2e-152;
                                     Indels
                                   0
                                   0; Mismatches
                                 478; Conservative
Query Match
Best Local Similarity
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AAU11644 standard; Protein; 478
                                                        (first entry)
                                                       12-MAR-2002
                                     AAU11644;
        AAU11644
RESULT
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121

QQ

The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen (CD80) for inducing the apoptosis of B7.2 antigen (CD80) for inducing the apoptosis of B7.2 antigen (CD80) for inducing the apoptosis of B7.2 antigen or accer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as indopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in human or animal and for treating or preventing resistance to or rejection of transplanted organ or fissue for treating proliferative antways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative collitis, food-related allergies e.g. migraine, chintis and eczema, and other types of allergies. The present protein sequence represents the heavy chain of 786, a primatised antibody ö GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120 YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY 180 9 Human; macaque monkey; light chain; primatised antibody; 7B6 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86; B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; Protein sequence of primatised form of the heavy chain of 7B6 antibody 1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as Gaps Length 478; 100.0%; Score 2561; DB 23; 100.0%; Pred. No. 4.2e-152; 0; Mismatches used in the invention to induce apoptosis interleukin-2; IL-2; mutant; mutein Example 8; Fig 4b; 89pp; English. Ġ, 22-MAY-2001; 2001WO-US16364 22-MAY-2000; 2000US-0576424 Matches 478; Conservative Chimeric - Homo sapiens. (IDEC-) IDEC PHARM CORP Hanna N, - Macaca sp WPI; 2002-089895/12. N-PSDB; AAS17245. Query Match Best Local Similarity 478 AA; WO200189567-A1. Anderson DR, 29-NOV-2001 Synthetic. Sequence 61 61 Chimeric allergy g Óγ g δ δ

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GenCore version 5.1.6
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OM protein - protein search, using sw model

2, 2003, 09:07:34; Search time 21.0061 Seconds (without alignments) 2188.349 Million cell updates/sec October Run on:

Perfect score:

US-09-758-173-8 2561 I MGWSLILLFIVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SS	Description	gamma-1 chain	gamma-3 chain	gamma-3 chain	gamma-2	4	snoclona	y heavy cha	gamma-2a cha	gamma-	y heavy chain	gamma-2a	gamma-2b	gamma-2b	gamma 2a	-	-	Ig gamma chain Cr	m	g gamma ch	gamma 3	by	Ig heavy chain C r	gamma-3 heavy	g gamma-1 c	gamma-2b	g gamma-1 chain	g gamma-3	g gamma-1 chain	ţ,
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Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig heavy chain pre	Ig heavy chain VHI	Ig Y heavy chain (Ig gamma-1 heavy c	Ig mu chain precur	Ig heavy chain (DO	1. T. Choire
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330	335 1	399 1	329	322	327	405	277	548	549	249	572	220	627	241	0.0
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43.8	43.7	43.6	43.5	43.3		42.2	41.5	39.4	33.7	32.4	31.1	31.1	30.1	29.6	

ALIGNMENTS

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SULT	HIO

1

RESULT 1
GHHU

Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: Aga33; Si861; S3187; B09563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82244238; PMID:6287432 '
A;Accession: A93433 MUID:82244238; PMID:6287432 '
A;Accession: A93433 MUID:82244238; PMID:6287432 '
A;Cross-references: EMBL:217370
A;Cross-references: EMBL:217370
A;Note: Lys-330 is removed after translation
B;Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S38661
A;Accession: S38661

A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 2-330 <HAR>
A; Cross-references: EMBL:217370
B; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A; Title: Structure of human immunoglobulin gamma genes: implications for evolution of A; Reference number: S33887; MUID:83001943; PMID:6811139
A; Accession: S33887

A.Molecule type: DNA
A.Coss-references: BMEL:217370
A.Clundingham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma
Biochemistry 9, 3161-3170, 1970
A.Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq
A.Mochents: myeloma protein Eu
A.Accession: B90563
A.Molecule type: protein Eu
A.Mocelle type: protein
A.Molecule type: protein
A.Mote: this sequence has the Glm(3) marker, 97-Arg
A.Mole: this sequence has the Glm(3) marker, 97-Arg
B.Mote: this sequence has the Mana gammaG-immunoglobulin. VIII. Amino acid se
A.Reference number: A90564; MUID:71064025; PMID:5530842

A)Contents: Eu A90564
A)Accession: A90564
A)Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Molecule type: protein A; Mesidues: 136-154, Q',156-165, Q',167-176, Q',178-194, N',196-197, D',199-238, E',2 A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met R; Ponstingl. H; Hilschmann, N. Hoppe-Seylar's Z. Physiol. Chem. 357, 1571-1604, 1976, A; Physiol. Chem. 357, A; Hille: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni A; Fittle: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni

us-09-758-173-8.rpr

```
ig gamma-3 chain C region (allotype G3m(b)) - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999 C;Datession: A2331 R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Niclei, Sev. 14, 1779-1789, 1986 A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A;Reference number: A23511; MUID:86148507; PMID:3081877
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g577056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPAVLQSS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMISRIPEVICVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH 341
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Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 ODWINGKEYKCKVSNKALPAPIEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVK
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C Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: immunoglobulin C; Keywords: immunoglobulin homology <IMM>
F;20-85/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C2
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A;Gene: GDB:IGHG3
A;Cross-references: GDB:119339; OMIM:147120
A;Map position: 14432.33-14432.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A;Title: A human immunoglobulin IGHG3 allele (GmbO, bl, c3, A;Accession: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
A;Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c3,
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Pred. No. 4.1e-89;
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F; 20-85/Domain: immunoglobulin homology <IMM>
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illarity 81,7%;
Conservative 1
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Best Local Similarity
Matches 308; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-377 <HUC>
                                                                                                                                                                                                                                                                                                                                                          A; Accession: A23511
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igen Primaerstruktur.

A; Reference number: A91668; MUID:77070269; PMID:826475

A; Contents: myeloma protein Nie

A; Accession: B91668

A; Molecule type: protein

A; Residues: 1.34, 'Q', 36-96', K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27

A; Note: this sequence has the Glm(17) and Glm(1) markers

R; Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

R; Rschmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 364, 713-774, 1983

A; Title: Die Primaerstruktur des Kristalisierbran monoklonalen Immunglobulins IgG1 KOL

A; Reference number: A91723; MUID:83289131; PMID:6884994

A; Contents: myeloma protein KOL; disulfide bonds

A; Accession: A91723

A; Molecule type: protein

A; Residues: 1.96, 'R', 98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330 < CER

A; Note: this sequence has the Glm(3) and Glm(non-1) markers

R; Rsidues: 1.96, 'R', 98-197,'D', 1970

A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfide

A; Contents: annotation; disulfide bonds

A; Contents: Pule of antibody structure. The primary structure of monoclonal IgG1 immunoglob

A; Title: Rule of antibody structure. The primary structure of monoclonal igG1 immunoglob

A; Reference number: A91667; MUID:700267; PMID:1002129
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A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32_33-14q32_33
A;Introns: 99/1; 114/1; 224/1
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% Search time 13.1847 Seconds
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1704.917 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: US-09-758-173-8
Perfect score: 2561
Sequence: 1 MGWSLILLFLVAVATRVQCE.....MHEALHNHYTQKSLSLSPGK 478

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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P01788 mus musculu	PO1790 mus musculu		P06337 mesocrice	PO1791 mus musculu	PO1792 mus musc	P04220 homo sap.	P01794 mus musci	P01764 homo sapien	-	P01801 mus musculu	P23087 heterodontu	
HV19_MOUSE	HV21_MOUSE	HV17_MOUSE	. MUC_MESAU	. HV22_MOUSE	. HV23_MOUSE	MUCB_HUMAN	HV25_MOUSE	HV3C_HUMAN	HV24_MOUSE	HV32_MOUSE	HVCS_HETFR	
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ALIGNMENTS

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SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
MEDLINE=82389131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
Three-dimensional structure determination of antibodies. Primary
structure of crystallized monoclonal immunoglobulin IgGl KOL, I.";
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                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDINCE OF 1-135 (MYELOMA PROTEIN EU).
MEDLINE=71064024; PubMed=5489771;
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Waxdal M.J., Edelman G.M.;
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                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1g gamma-1 chain C region.
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SEQUENCE OF 136-329 (EU).
MEDLINE=71064025; PubMed=5530842;
                                     STANDARD;
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                                                                                                             Dreker L., Schwarz J., Reichel W., Hilschmann N.; Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's 2. Physiol. Chem. 357:1515-1540(1976).
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GO; GO:0003823; F:antigen binding activity; TAS.
GO; GO:0003825; F:immune response; NAS.
Interpro; IPR003597; Ig_c1.
Interpro; IPR003597; Ig_c1.
Ffam; PF0047; Ig_ 3.
SWARY; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_LIKE; 3.
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HINGE.
CH2.
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                                                                      DISULFIDE BONDS.
MEDLINE=77070267; PubMed=1002129;
    Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PDB; 1FC2, 15-JUL-92.
PDB; 1FC2, 15-JUL-92.
PDB; 1D53; 12-NUV-97.
PDB; 1D58; 09-FEB-00.
PDB; 1D57; 09-FEB-00.
PDB; 1D57; 09-FEB-00.
PDB; 1D7; 10-NUV-97.
PDB; 1D7; 10-NUV-01.
PDB; 1FCC; 20-JUL-92.
PDB; 1TX; 16-NAY-01.
PDB; 1IX; 16-NAY-01.
PDB; 2RCS; 12-NUV-97.
GENEW; HGNC:5525; 1GHG1.
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3D-structure.
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DOMAIN 1 98
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MIM; 147100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 GLYSLSSVYTVPSSSLGTQTYICHVHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                                             EMOVED POST TRANSLATIONALLY.

K -> R (IN GlM(3) MARKER).

/FTId=VAR_003886.

D -> E (IN GlM(NON-1) MARKER).

/FTId=VAR_003887.

L -> M (IN GlM(NON-1) MARKER).

/FTId=VAR_003888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 330;
INTERCHAIN (WITH LIGHT CHAIN)
INTERCHAIN (WITH HEAVY CHAIN)
INTERCHAIN (WITH HEAVY CHAIN)
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Pred, No. 1.2e-117;
0; Mismatches 1;
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68 GFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT----TSY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAPGKGPEWV
098wk1 homo og 096k68 homo og 08 ved mus men og 095k8 homo og 095k8 hus men og 095k8 hus men og 095k8 homo og 095k
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Q8vcv5 mus n
Q8vcx4 mus n
Q99la6 mus m
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.1%; Score 2178.5; DB 4; Length 471; Best Local Similarity 87.2%; Pred. No. 1.4e-180; Matches 416; Conservative 15; Mismatches 27; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straugherg R.;
Straugherg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC024289, AAHJ2989.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00306; Ig_W.
Pfam; Pr00406; Igv.
RNART; SM00406; IGv; 1.
PROSITE; PS00895; IG_LIKE; 4.
PROSITE; PS00890; IG_MHC; 2.
Hypothetical protein.
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471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Last sequence update)
Last annotation update)
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098WUKI
096K68
086K68
096GA6
092IKI
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091WP5
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091XD1
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091XD1
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09BU10
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Q96EY0
Q8WUX4
Q96AA6
Q8K0F2
Q91WR1
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Q8VCX4
Q99LA6
Q91WT3
Q91X92
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TISSUE=Spleen;
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TC77
Q8TC77;
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Q8TC77
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Q8n4y9 homo sapien
Q8tc63 homo sapien
Q8r3v9 mus musculu
Q8nf17 homo sapien
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(without alignments)
2666.544 Million cell updates/sec
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2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
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                                                                                                      2, 2003, 08:56:23;
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Maximum Match 100%
Listing first 45 summaries
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Q8N4Y9
Q8TC63
Q8R3V9
Q8R3V9
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_tungi:*
sp_tungi:*
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sp_invertebrate:*
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
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Match Length
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Perfect score:
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Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025985; AAH25985.1;
InterPro; IPR000923; Bluecu_1.
InterPro; IPR000923; Bluecu_1.
InterPro; IPR000906; Ig-like.
InterPro; IPR003506; Ig_WHC.
InterPro; IPR003596; Ig_V.
SMART; SM00406; IGV; 1.
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Last annotation update)
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$; Pred. No. 5.1e-151;
33; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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75.5%;
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SEQUENCE 473 AA;
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Matches 357; Conserv
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01-JUN-2002 (
01-MAR-2003 (
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                                                       301
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                                                                                                                          PEPVIVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
                                                                                                                                                                       175 PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK
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Catarrhini, Hominidae, Homo.
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EMBL; BC033178; AAH33178.1; -
InterPro: IPR00710; Ig-like.
InterPro: IPR003597; Ig_c1.
InterPro: IPR003597; Ig_c1.
InterPro: IPR003006; Ig_MEC.
InterPro: IPR003596; Ig_v.
Pfam; PF00047; Ig1 4.
SMART; SM00407; IG21; 3.
SMART; PS00406; IGV; I.
PROSITE; PS00299; IG_LIKE; 4.
PROSITE; PS00299; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 82.1%; Score 2103.5; DB 4; 21 Similarity 76.4%; Pred. No. 5.1e-174; 401; Conservative 27; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521
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TISSUE-Primary B-Cells from Tonsils;
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Mammalla; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Hyporhetical protein, Homo sapiens (Human).
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Submitted (JU
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FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNT 236
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                                                                                                               KVDKRVELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDT
                                                                                                                                                                      254 THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF\WYVDGV
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                 LENGIH: 478 amino acids
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US-08-487-550-8
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Sequence 8, Appli
Sequence 71, Appl
Sequence 71, Appl
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                                                                                                      2003, 09:12:09 ; Search time 21.2295 Seconds (without alignments) 952.662 Million cell updates/sec
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Sequence 18,
Sequence 2, A
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2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
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Sequence 14,
Sequence 16,
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Sequence 2,
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Sequence 8
Sequence 8
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    /cgn2_6/ptodata//iaa/5A_COMB.pep:*
    /cgn2_6/ptodata//iaa/5B_COMB.pep:*
    /cgn2_6/ptodata///iaa/6A_COMB.pep:*
    /cgn2_6/ptodata///iaa/6B_COMB.pep:*
    /cgn2_6/ptodata//iaa/PCTUS_COMB.pep:*
    /cgn2_6/ptodata//iaa/pcTUS_COMB.pep:*
    /cgn2_6/ptodata//iaa/pcTUS_COMB.pep:*
    /cgn2_6/ptodata//iaa/pcTUS_COMB.pep:*
                5.1.6
Compugen Ltd.
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                  GenCore version (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 200000000
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Maximum DB
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Sequence 8, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONNEW MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "O HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACHUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: PHARMACHUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: PHARMACHUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: MANUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: VA
CONTREST: VA
CONTRY: USA
CONTRY: USA
ZIP: 22314
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MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE:
COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
COMPATIBLE
CLASSIFICATION NUMBER: US/08/487,550
FILING DATE: 07-7UN 1995
CLASSIFICATION NUMBER: US/08/487,550
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, ROBIN L.
REGISTENCE/DOCKET NUMBER: 012712-131
TELEPROCOMMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION 1870-1836-2021
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US-08-793-450-8

US-09-740-002-25

US-09-526-098-4

US-09-301-20-27

US-09-301-593-43

US-09-301-593-43

US-08-397-411-7

US-09-397-411-7

US-08-397-411-7

US-09-301-593-30

US-09-301-593-30

US-09-301-593-30

US-09-301-593-30

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US-09-301-301-301-301

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Gaps

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us-09-758-173-8.rai

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GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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                                                                                                      Gaps
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APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta. Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SOURNESS: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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0
                                                            Length 478;
                                                                                                   Indels
                                                            Score 2561; DB 4;
Pred. No. 1.2e-198;
0; Mismatches 0;
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHWARE: Winbatin (Generical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,449
FILING DATE: 20-Feb-1998
CLASSIFICATION DATA:
RAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/09027449 Patent No. 6025158
                                                            100.08;
100.08;
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1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                            Query Match
Best Local Similarity 100.
Matches 478; Conservative
    protein
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, MOLECULE TYPE:
US-09-526-098-8
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Sequence 8. Application US/09526098
Sequence 8. Application US/09526098
Sequence 8. Application Sequence 8. Sequence 8. Sequence 8. Sequence 8. Sequence 8. TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: "MONKEY MONOCLONAL AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: INMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PRINCE Street
CITY: Alexandria
                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVXYCTTS 120
                                       GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
                                                                                180
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                                                                                                                                                                                                                                                                  DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP 360
                                                                                                                                                                                                                                                                                                                                                                                                           APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
                                                                                                                                                                                                                                                                                                                                                                                                                                NYKTIPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121. YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                              FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
                                                                                                                                                                                      181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVHKPSNT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-40N-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET VUMBER: 012712-131
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARATTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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US-09-526-098-8
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421.442 Million cell updates/sec
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                                                                                                                                                                                US-09-758-173-8
2561
1 MGWSLILLFLVAVATRVQCE......MHEALHNHYTQKSLSLSPGK 478
                                                                                                          2, 2003, 09:18:44 ; Search time 179.446 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-948-429B-8
US-10-124-807-8
US-10-218-32-8
US-10-124-905-8
US-09-726-258-71
US-09-725-108A-3
US-10-225-108A-3
US-10-020-786-9
US-10-020-786-9
US-10-227-694-5
US-09-822-698A-26
US-09-736-371B-21
US-09-736-371B-21
US-09-736-371B-21
US-09-736-974-5
US-10-20-786-11
US-09-736-974-12
US-09-736-974-12
US-09-825-012-45
US-10-386-974-2
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Maximum Match 100%
Listing first 45 summaries
                                                                       protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Perfect
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        Sequence 2, Appli

        17
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        US-10-365-694-2
        Sequence 2, Appli

        19
        2144.5
        83.7
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        10
        US-09-825-012-61
        Sequence 61, Appli

        20
        2138.5
        83.5
        740
        10
        US-09-825-012-8
        Sequence 61, Appli

        21
        2137.5
        83.4
        451
        12
        US-10-150-475A-6
        Sequence 18, Appli

        22
        2135
        83.4
        451
        12
        US-10-150-475A-6
        Sequence 18, Appli

        24
        2135
        83.4
        451
        12
        US-10-13-96-18
        Sequence 18, Appli

        25
        2135
        83.4
        451
        12
        US-10-36-2
        Sequence 15, Appli

        26
        2135
        83.4
        470
        12
        US-10-36-2
        Sequence 15, Appli

        27
        2135
        83.4
        471
        15
        US-09-925-179-6
        Sequence 16, Appli

        28
        2135
        83.2
        451
        US-09-92
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ALIGNMENTS

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1S-09-944-429B-8

1S-09-944-429B-8

Sequence & Application US/09948429B

Sequence & Application US/09948429B

Patent No. US20020177689AI

Patent No. US20020177689AI

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARMACEVITAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

TORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: VA

CONTRY: USA

CONTRY: USA

COMPTRY: USA

COMPTRY: Exabable FORM:

WEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

WEDIUM TYPE: Floppy disk

COMPUTER: DATE:

COMPUTER: DATE:

MEDIUM TYPE: Floppy disk

COMPUTER: DATE:

SOFTWARE: PATENTION DATA:

APPLICATION NUMBER: US/09/948,429B

FILING DATE:

CLASSIFICATION NUMBER: US/09/948,550

FILING DATE:

PRIOR APPLICATION NUMBER: 35,030

FILING DATE:

REFERENCE/DOCKET NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

TELECOMMUNICATION NUMBER: 35,030

TELECOMMUNICATION NUMBER: 1012712-131

TELECOMMUNICATION NUMBER: 35,030
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REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                   US 08/487,550
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,556
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: TESKID, ROBIN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 8, Application US/10291532; Publication No. US20030180290A1; GENERAL INFORMATION:
                                                                                                   NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                                                                                                                                                                                    INFORMATION FOR EGO ID NO:
SEQUENCE CHRACTERISTICS:
LENGTH: 478 amino acids:
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                              ) MOLECULE TYPE: protein US-10-124-807-8
                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                    TOPOLOGY:
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US-10-291-532-8
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 420
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                                                                                                                                                                                                                                      1 MGHSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                  61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                                                                                                                                                                                                                                                                                                                     181 FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNT
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                                                                                                                                                                                                                  1 MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                                                61 GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS
                                                                                                                                                                                                                                                                                                                                                   YISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDY
                                                                                                                                                    Length 478;
                                                                                                                                                                                    Indels
                                                                                                                                               100.0%; Score 2561; DB 10;
100.0%; Pred. No. 1.2e-169;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Publication No. US20030166207A1
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               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                Matches 478; Conservative
 703-836-2021
                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                               amino acid
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                                                                                                                                                                  Best Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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   TELEFAX:
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241 KVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE 300
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APPLICAMY: HANNA, NABIL
APPLICAMY: HANNA, NABIL
TITLE OF INVENTION: ANTI-CDE0 ANTIEDDY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TILE REPRENCE: 037003/291872
CURRENT APPLICATION NUMBER: 05/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/31,187
PRIOR APPLICATION NUMBER: 09/758,173
                                                                                                                                                                                                                       GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCTTS 120
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October 2, 2003, 13:01:50; Search time 1867.6 Seconds (without alignments) 15574.362 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

۵	AR108866 Sequence AR265200 Sequence	BD063038 Identific	AR135362 Sequence AB064208 Homo sapi	BD176841 A method x14583 Human mRNa	BC020233 Homo sapi	ABU04143 HOMO Sapi AB064188 Homo sapi	BC022098 Homo sapi AB064149 Homo sapi	AB064148 Homo sapi	ABU0414/ HOMO Sapi AB064219 HOMO Sapi	X57817 Human rearr	ABO64141 Homo sapi	AB064227 Homo sapi AB064172 Homo sapi	AB064206 Homo sapi	X57811 Human rearr	AB064150 Homo sapi AB064169 Homo sapi	AB064166 Homo sapi	ABU642U3 HOMO Sapi AB064171 HOMO Sapi	AB064170 Homo sapi	ABU04151 HOMO Sapt BD078409 Antigen-b	BD078410 Antigen-b	ABU04216 HOMO Sapi AB064222 Homo sapi	AB064218 Homo sapi	X57822 Human rearr	X57815 Human rearr	AX287808 Sequence	AB064205 Homo sapi BC012876 Homo sapi	ו מזי	sap 10e		1000-dag- ht mkd receif	GT 1 1 101 1501			sstowsky,W.S. and Heard,C.	transiect
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% t Cuery . Score Match Leng	7	711 100.0	582.6 81.9 9 575.4 80.9 7	573 80.6 8	571.2 80.3	9 5/0.6 80.3 8 0 566.6 79.7 8	566.4 79.7 9 566 79.6 8	3 562.8 79.2 8	5 562.4 79.1 8	6 562.2 79.1 7	8 558 78.5	9 558 78.5 8 0 557.6 78.4 8	1 556.4 78.3 7	3 555.4 78.1 8	5 554.8 78.0 8 5 554.4 78.0 7	6 554.4 78.0 8	8 552.8 77.7 7	9 552.8 77.7 7	1 552.6 77.7 7	2 552.6 77.7 7	3 351.6 77.4 8	5 548.4 77.1 8	7 547.8 77.0 8	8 546.2 76.8 8 0 546.2 76.8 8	0 545.6 76.7 94	1 545 76.7 7 2 541 76.1 9	3 540.8 76.1 6	4 540.4 /5.0 B 5 540.2 76.0 7		1 56 350 3510096	TION Sequence 9 f	AKIU8800.1 GI	Unknown. Unknown. Hoolassifi	, 7 %	Human B7.1 expressing Patent: US
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FEATURES Location/Qualifiers source 1.711 DASE COUNT 160 a 226 c 193 g 132 t ORIGIN Query Match 100.0%; Score 711; DB 6; Length 711; Heart Local similarity, 100.0%; Dred No 6, Re-174.	111 Conservative	Db 61 GAGTCTGTCTGACAGCCCCTCTGGGGGCCCCAGGGCAGAGGTCACCATC 120	QY 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300 Db 241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300 QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCCTGAATGCTCAGGTA 360 Db 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCCTATGACAGCCTGAATGCTCAGGTA 360	Qy 361 TTCGGAGGAGGACCGGCTGACCTCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACT 420	QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCCGGTCAAG 540	Qy 601 TACCTGAGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGGTGCCAGGTCACG 1	RESULT 3 BD063038 LOCUS DEFINITION Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens. ACCESSION BD063038 ACCESSION BCFCBCCOSTIMULATOR ACCESSION BCFCBCCOSTIMULATOR ACCESSION BCFCBCCOSTIMULATOR ACCESSION BCFCBCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCOSTION BCFCBCCCCOSTION BCFCBCCCCOSTION BCFCBCCCCOSTION BCFCBCCCCOSTION BCFCBCCCCCOSTION BCFCBCCCCOSTION BCFCBCCCCCCOSTION BCFCBCCCCCCCCCOSTION BCFCBCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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Human benign prost Lung cancer relate Human immune syste Human iga anti-rhe Human iga anti-rhe Human iga anti-rhe Human type antihum Plasmid scPv(CC046 Human type antihum Human hype antihum Human polynucleoti DNA encoding novel Human polynucleoti DNA encoding novel Human prostate exp Human immune syste Human prostate exp Human prostate exp Human secreted prostate exp Human secreted prostate of Human secreted prostate brown secreted prostate and Human secreted prostate exp Human Human
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DNA sequence of a
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/product= 16C10 light chain
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Plasmid Glambda-1B
Plasmid Glambda-1B
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                 GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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Scoring table:

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29-OCT-1997; 08-NOV-1996;

Score

Result Š. 709.4 582.6 573 571.4 565.2 558.8

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Human; macaque monkey; light chain; primatised antibody; 16C10 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; PT_1 antigen; CD80; PT_2 antigen; CD80; B Cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA.sequence of a primatised form of the light chain of 16C10 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CDB6) and/or B7.2 antigen (CDB6) for inducing the appross of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leuksemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoia arthritis, psoriasis, aplastic anaemia, inflammatory bile diseases, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression
                                                           AGTGACTTCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCCGTCAAG
                                                                                                                TACCTGAGCCTGACGCCTGAGCAGTGGAAGTCCCACAGAAGCTACAGCTGCCAGGTCACG
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                                                                                                                                                                                         661 CATGAAGGGAGCACCGTGGAGAAGACAGTGGCCCCTACAGAATGTTCATGA 711
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/product= "Light chain of 16C10 antibody"
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                                                                                                                                                                                                                                                               This sequence encodes a primatized form of the antibody 16C10 light chain from macaque. This sequence is used in a method which studies new monclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antiqens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell's eall interactions, particularly autoimmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, infections with the service of inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumnours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-ddictype reagents and as vaccines or immunogens to develop anti-ddictype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and inhibits antigen-specific immunoglobulin G (19G) responses.
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                                          Hanna N;
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2, 2003, 13:05:20 ; Search time 1175.83 Seconds (without alignments) 14696.420 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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711 1 ATGAGGGTCCCCGCTCAGCT......CCCCTACAGAATGTTCATGA 711 22781392 seqs, 12152238056 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Title: Perfect score: Sequence: Scoring table: Searched:

US-09-758-173-9

45562784 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

em_estba:* EST:* Database :

em_gss_phg:* em_gss_vrl:* gb_gssl:* gb_gss2:* em_gss_pro:* em_gss_rod:* em_gss_mus:* em_gss_hum:* em_esthum:
em_esthum:
em_esthu:
em_estov:
em_estpl:
em_estro:
em_btc:
gb_estl:* em_estfun: em_dss_pln: em_gss_mam: gb_est4:* gb_est5:* gb_est2: qb_htc:* Jp_est3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	BQ711292 AGENCOURT BQ708635 AGENCOURT BQ708570 AGENCOURT BG685644 602637629	
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& Query Match	80.1 79.1 78.6 78.6	
sult Query No. Score Match Length DB ID	569.2 562.6 559 559	
Result No.	H 01 W 4*	

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ALIGNMENTS

BQ711292 956 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8353826 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6278335 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 956)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2466 row. c column: 08
High quality sequence start: 10 5', mRNA sequence. BQ711292 BQ711292.1 GI:21850191 Homo sapiens (human) Homo sapiens ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 BQ711292 LOCUS DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/lab_host="Delign () phage-resistant)"
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/clone_lib="NIH_MGC_113"
/note="Corgan: Spleen; Vector: pdfB; Site_1: XhoI; Site_2: BcoRI; cDNA made by olign of Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a 30 c Library. I others
                                         BQ708635 913 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312
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NIH-MGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MG clone distribution information can bfound through the I.M.A.G.E. Consortium/LLNL at:
http://maqg.llnl.gov
Plate: LLCM2476 row: i column: 01
High quality sequence stop: 663.
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Pred. No. 1.9e-128;
0; Mismatches 75;
                                                                                                                                                                                                                                                                       Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
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/clone="IMAGE:6282312"
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                                               /organism="Homo sapiens"
//organism="Homo sapiens"
//mol_type="mRNA"
//do_type="mRNA"
//do_tef="twan:9606"
//clone="Inkage:6278335"
//lab_host="DH10B (phage-resistant)"
//clone="lb="NIH" MGC_113"
//note="Organ: spleen; Vector: poTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Homy in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
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Pred. No. 4.5e-130;
0; Mismatches 78;
High quality sequence stop: 655.
Location/Qualifiers
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Local Similarity 88.6%;
Nes 629; Conservative
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence Seq Seguence

US-08-761-277A-50

ALIGNMENTS

US-08-487-550-9

, Dairell R. "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESANTS" Sequence 9, Application US/08487550
Patent No. 6113898
GENERAL THRORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOLY
TITLE OF INVENTION: PHARMACEUTIAL
TITLE OF INVENTION: PHARMACEUTIAL
TITLE OF INVENTION: IMMUNOSUPPRESA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

3: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street Alexandria ٧A ADDRESSEE: STREET:

USA

COUNTRY:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy 22314

FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: TESKIN, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-2021

711 base pairs nucleic acid INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: STRANDEDNESS

not relevant

CDS 1..711 linear MOLECULE TYPE: NAME/KEY: LOCATION: FEATURE:

mat_peptide 1..711 , NAME/KEY; ; LOCATION; US-08-487-550-9

, Length 711; DB 3; Score 711; 100.08; Query Match

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

569978 seqs, 220691566 residues

Searched:

Issued_Patents_NA:*

... /cgn2_6/ptodata/2/ina/5A_COMB.seg:*
... /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
... /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
... /cgn2_6/ptodata/2/ina/B_COMB.seq:*
... /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
... /cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
... /cgn2_6/ptodata/2/ina/Packfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Sequence 9 populi	to educate		equence 1.	equence 1.		m	23	Ξ	Sequence 47, Appl	50	l.	24	46,	970	970	551,	'n	83.	833,		908	268	268	268,	158	1589,
SUMMARIES		ID	US-08-487-550-9	US-09-526-098-	US-09-049-672A	US-08-487-5	US-09-526-	-09-049-672	-09-372-	70-60-	-08-3	-09-1	-09-1	US-08-523-894-5	70-60-	-60-	-60-	-60-	-09-620-313	-80-	-09-702-705	US-09-736-457-833	-09-702-	US-09-736-457-908	US-09-404-879A-268	US-09-338-933-268	-09-215-681-26	US-09-702-705-1589	US-09-736-457-1589
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PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                        : 711 base pairs
nucleic acid
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Matches 711; Conservative
                                    DATA
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                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                       SOFTWARE: Patentin
CURRENT APPLICATION DA
APPLICATION NUMBER:
           OPERATING SYSTEM:
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LOCATION:
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COCATION:
US-09-526-098-9
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Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF PITTLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SECUENCES: 12
CORRESPONDENCE ADDRESS:
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                       Indels
           Pred. No. 2.6e-186;
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                      Mismatches
100.08; ±4.001
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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       Best Local Similarity 100. Matches 711; Conservative
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REGISTRATION NUMBER: 35,030
REPERSUCE/DOCKET NUMBER: 0127:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

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2, 2003, 19:53:01; Search time 140.653 Seconds (without alignments) 12894.584 Million cell updates/sec
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Maximum Match 100%
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13206, A 4, Appli 5, Appli 4, Appli 5, Appli 70, Appli Appli Appli Appli Appl 799, Sequence Sequence Sequence Sequence Sequence 1 Sequence 4 Sequence 5 Sequence 4 Sequence 5 Sequence 7 Sequence Sequence Sequence Description Sequence Sequence Sequence US-10-124-807-9 US-10-291-532-9 US-10-073-138-5 US-10-198-846-13206 US-09-747-669-4 US-10-290-703-4 US-10-290-703-4 US-10-158-646-70 US-10-198-846-12799 US-10-158-646-71 US-09-948-429B-1 US-10-124-807-1 US-10-291-532-1 US-09-948-429B-9 SUMMARIES Query Match Length DB Score 5501.8 5552.6 5552.6 5552.6 5552.6 5552.6 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 550.0 Result Š O

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ALIGNMENTS

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Anderson, Darrell R.
VENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
VENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
VENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
VENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                    BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                     Sequence 9, Application US/09948429B Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35,030
                                                                                                                                                                                                                                                  ADDRESSEE: BURNS, DOANE, S
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Teskin, Robin L.
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                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                 GENERAL INFORMATION:
APPLICANT: Anders
                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                  22314
US-09-948-429B-9
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                      STATE:
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1, Darrell R. "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESANTS"

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
                                                                                                                                                     ZUP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
-REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 711 base pairs
nucleic acid
EDNESS: not relevant
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                TITLE OF INVENTION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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LOCATION:
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                                                                                                                                                                                           Score 711; DB 10;
Pred. No. 5.4e-206;
Mismatches 0;
                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; P
Matches 711; Conservative 0;
                       : 711 base pairs
nucleic acid
EDNESS: not relevant
SEQUENCE CHARACTERISTICS:
                                                                                                                                          mat_peptide
                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                 1..711
                                                 STRANDEDNESS:
                                                                                                   NAME/KEY:
LOCATION:
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; LOCATION:
US-09-948-429B-9
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US-10-124-807-9
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CCAGGAACGGCCCCCAAACTCCTCATCTATGACATTAACAAGCGACCCTCAGGAATTTCT 240
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                                                                                                                                          GAGTCTGTCCTGACACACCCCCCCTCAGTGTCTGGGGCCCCCAGGGCAGAAGGTCACCATC
                                                                                           1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT
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                                                                      1 ATGAGGGTCCCCGCTCAGCTCCTGGGGCCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGT
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 Length 711;
                                    Indels
 Score 711; DB 12;
Pred. No. 5.4e-206;
Mismatches 0;
100.0%; Sillarity 100.0%; P. Conservative 0;
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Sequence 9, Application US/10124807 Publication No. US20030166207A1 GENERAL INFORMATION:

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(IDEC-) IDEC PHARM CORP
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Moncolonal antibod
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Human anti-TIMP-1
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| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSI/gcddata/geneseqp-embl/AA1981.DAT:*
| SIDSI/gcddata/geneseqp-embl/AA1984.DAT:*
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| SIDSI/gcgdata/geneseqy-embl/AA2001.DAT:*
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1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 236
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                  1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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Human anti-TIMP-1	148	24	$\dot{\mathbf{H}}$	9	47.	37
nti-TIMP-	48	24	$\vec{\Box}$	7	48.	36
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Human anti-TIMP-1	48	24	$\dot{\Box}$	7	•	34
Human anti-TIMP-1	6	24	$\dot{\mathbf{H}}$	7.	50.	33
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immune	521	22	3	8	96	21
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Anti-HIV-1 recombi	9	14	\vdash	σ.	9.	13
Human anti-TIMP-1	9 7	24	Н	о О		12
Human polypeptide	39	23	φ	ö	ထ	11
Human anti-TIMP-1	47	24	_	0	œ	10

Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation. Macaque primatized 16C10 light chain protein. AAW63764 standard; Protein; 236 AA 96US-0746361 97WO-US19906 29-SEP-1998 (first entry) Macaca fascicularis 29-OCT-1997; 08-NOV-1996; WO9819706-A1 14 - MAY - 1998

Hanna N;

Brams P,

WPI; 1998-286601/25. N-PSDB; AAV35488.

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This sequence represents a primatized form of the antibody 16C10 light chair sequence represents a primatized form of the antibody 16C10 light chair from macaque. This sequence is used in a method which studies new monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such mab's are specific immunosuppressants for treatment of diseases involving a clopathic thrombocytopaenia parputa, systemic lupus erythematosus, type idiopathic thrombocytopaenia parputa, systemic lupus erythematosus, type idiopathic thrombocytopaenia parputa, systemic lupus erythematosus, type idiopathic thrombocytopaenia parputa, systemic lupus erythematosus, concern fost diseases, a leafy and multiple solerosis, graft vs. Inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the NAb can be conjugated to a drug or toxin. MAb's, or their fragments, can also be used as imaging agents and as vaccines or immunosques to develop anti-idiotype reagents. MAb's are optionally combined with other proteins or small molecule immunosuperessants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuperession, i.e. it inhibits antigen-specific immunosuperses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, macaque monkey, light chain, primatised antibody, 16C10 antibody, neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86; B7_2 antigen; CD86, B Cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRVPAQLLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between I and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1232; DB 19; Length 236; 100.0%; Pred. No. 1.2e-66; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    graft-vs-host disease; immunosuppression; organ rejection;
interleukin-2; IL-2; mutant; mutein.
                                                                                                                             5a; 87pp; English,
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The present invention relates to a new use of a monoclonal antibody which specifically binds to B7.1 antigen (CDB0) and/or B7.2 antigen (CDB0) for inducting the apoptosis of B7+ cells. The invention is useful for treating the apoptosis of B7+ cells. The invention is cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as Grinopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple solercisis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted organ or tissue for treating reversible obstructive and hyperproliferative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative diseases, for treating reversible obstructive airways disease, intestinal inflammations and allergies e.g. Crohn's disease and ulcerative colitis, food related allergies e.g. migraine, chinitis and eczema, and other types of allergies. The present protein sequence represents the light chain of 16ClO, a primatised antibody used in the invention to induce apoptosis and inhibit production of

interleukin-2 (IL-2).

Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as

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Brams

WPI; 2002-089895/12 N-PSDB; AAS17246

Anderson DR,

(IDEC-) IDEC PHARM CORP

22-MAY-2001; 2001WO-US16364 22-MAY-2000; 2000US-0576424

29-NOV-2001.

Example 8; Fig 5a; 89pp; English

allergy

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PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                                                                                                                                                                                                  100.0%; Score 1232; DB 23; Length 236; 100.0%; Pred. No. 1.2e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primatised anti-human B7.1 antigen antibody 16C10 light chain.
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ses 236; Conservative
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WO200189567-A1 Synthetic.

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Rixishimoto, T. S05270

A; Accession: S05270

A; Coss.references: EMEL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

A; Cross.references: EMEL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

A; Cross.references: EMEL:X14583

A; Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains A; Reference number: S04601; MUID:89296497; PMID:2500644

A; Accession: S04601

A; Molecule type: mRNA

A; Residues: 1-130 < KISS.2

A; Cross-references: EMEL:X14583

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Superfamily: immunoglobulin v region; immunoglobulin

F; 1-20/Domain: signal sequence #status predicted <AAT>
F; 120-218/Domain: immunoglobulin homology <IMM>
F; 121-235/Product: Ig lambda chain #status predicted <AAT>
F; 150-218/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                        ALIGNMENTS
                     S70431
S170220
S17399
S17399
S17449
PC41177
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Maximum Match 100%
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Ig lambda chain V region - human
C; Species: Homo sapiens (man)
C; Date: 19-War-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C; Species: Homo sapiens (man)
C; Date: 19-War-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jan-2000
C; Accession: 829258
R; Chouchane, L; Van Spronsen, A; Breyer, J; Guglielmi, P.; Strosberg, A.D.
Bur. J. Blochem. 207, 1115-1121, 1992
A; Reference number: 829257; MUID:92362614; PMID:1499555
A; Reference number: 829257; MUID:92362614; PMID:1499555
A; Reterence number: 829257; MUID:92362614; PMID:1499555
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A; Reterence number: 829257; MUID:92362614; PMID:1499555
A; Rocession: 829257; MUID:1920**
A; Rocession: 829257*
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Lano sapiens (man)
R.Combriato, G.; Klobeck, H.G.
R. Species: No. 1513-1513, 1991
A.Reference number: S16439; MUID:91257162; PMID:1904362
A.Status: preliminary; translation not shown
A.Status: preliminary; translation not shown
A.Status: RNA
A.Residues: 1-234 < COM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVLTQPPSVSGAPGQRVTISCTGSSSNIGARYDVNWYQQLPGTAPKLLIYGNTRPSGV
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Kikuyoords: heterotetramer: immunoglobulin homology 
Kikuyoords: Immunoglobulin homology 
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L.6e-58;
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Pred. No. 1.6e
9; Mismatches
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ilarity 89.9%;
Conservative
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Local Similarity 83.0%;
hes 191; Conservative 2
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Best Local Similarity
Matches 195; Conserv
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C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: $25746
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda) -C(lambda) gene segments of the human immuno
A;Reference number: $16439; MUID:91257162; PMID:1904362
A;Reference number: $25746
A;Reference number: $25746
A;Reference number: $16439; MUID:91257162; PMID:1904362
A;Reference number: $16439; MUID:91257162; PMID:190
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C;Accession; 255752
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(Lambda) and J(lambda) "C(lambda) gene segments of the human immuno A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: 825752
A;Actus: preliminary; translation not shown
A;Residues: 1-233 <COM>
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MEDLINE-95255298; PubMed=7737190;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
Shimizu A.;
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                                                                                                                                                                                                 LAC_HUMAN STANDARD; PRT; 105 AA. P01842; P80423; L1-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 16-CL AND IGLC2 AND IGLC3.
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LV3A_HUMAN

LV6E_HUMAN

LV6E_HUMAN

KV1J_HUMAN

KV1J_HUMAN

LV4E_HUMAN

LV5A_HUMAN

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LV4E_HUMAN

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Biochem. J. 110:631-652(1968).
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-I- MISCELLANEOUS: THE SEQUENCE SHOWN IS THE KERN-/OZ-/MCG- CHAIN FOUND IN PROTEINS SH, X, AND NIG-64. THE KERN PROTEIN HAS THE KERN PROTEIN HAS THE MARKER, THE MCG PROTEIN HAS THE KERN+ MARKER.

-I- MISCELLANGOUS: SIX TANDEM LAMBDA TYPE GENES WERE IDENTIFIED & THE 3 MOST 5' WERE SEQUENCED. THESE CORRESPOND TO THE MCG SEQUENCE (LAMBDA-1), THE KERN-/OZ- SEQUENCE (LAMBDA-2) & THE KERN-/OZ+ SEQUENCE (LAMBDA-2) & THE KERN-/OZ+
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MEDLINE-82080680; PubMed=6273747;
Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90133913; PubMed-2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in
water. Conformational flexibility of a molecule in two crystal
                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
MEDLINE-75046825; Pubmed-4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
                                                                                                                                                                                   the fab' fragment of a human
Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panaglotopoulos N.;
"Rotational allomerism and divergent evolution of domains in
"munuoglobulin light chains.";
Biochemistry 14:3953-3961(1975).
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                                                                                                                                                             Saul F.;
"The three-dimensional structure of the fab' fragmyeloma immunoglobulin at 2.0.A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
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Fett J.W., Deutsch H.F.;
"Primary structure of the Mcg lambda chain.";
Blochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
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EMBL, 138562; AAB36581.1; ALT_INIT.
EMBL, X51754; CAB36569.1; ALT_INIT.
EMBL, X51755; CAA36049.1; -.
EMBL, X51755; CAA36051.1; -.
                                            3ur. J. Biochem. 228:886-893(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol. 210:601-615(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY OF MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A92057; L2HU.
2MCG; 15-JUL-92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 7FAB; 31-JAN-94.
PDB; 1AQK; 04-FEB-98.
PDB; 1LIL; 15-MAY-97.
                        immunoglobulins.";
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Nature 29
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132 QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTPSKQ 191
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pram; Pr00047; Ig; 1.
SMART; SW00407; IGc1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MIC.; I_MIC.; I_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Lambda-like polypeptide | precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
(CD179b antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McKearn J.P.;
"Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
expressed in pre-B cells and may encode the human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-89315835; PubMed-2501791;
Hollis G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
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/FIId=VAR_003898.
5 -> T (IN MCG+ MARKER).

/FIId=VAR_003899.
5 -> G (IN KERN+ MARKER).

/FIId=VAR_003900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCD9C7C201C13CC2 CRC64;
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/FIId=VAR_003901.
R -> K (IN OZ+ MARKER).
/FIId=VAR_003902.
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100.0%; Pred. No. 1.2e-36;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 105; Conservative
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Q91w12 mus musculu QBr062 mus musculu QBvc16 mus musculu Q99m37 mus musculu Q91w48 mus musculu Q81w63 homo sapien Q8vc55 mus musculu Q8rc028 mus musculu Q8r028 mus musculu
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Elwayota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
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TISSUB-TONSI;

Strausberg R.;

Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; BC020233; AAH20233.1;

InterPro; IPR003065; Ig_MHC.

InterPro; IPR003065; Ig_V.

Pfam; PF00047; Igy 2.

SMART; SM00406; IGV: 1.

PROSITE; PS00290; IG_MHC; 1.

PROSITE; PS00290; IG_MHC; 1.

PROSITE; PROTetical protein.

SEQUENCE 237 AA; 24897 MW; 73C7D70B6039D186 CRC64;
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84.8%; Score 1045; DB 4; Length 2
Best Local Similarity 88.4%; Pred. No. 2.2e-83;
Matches 205; Conservative 10; Mismatches 15; Indels
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                                                                  099M37
091W89
091W89
08TE63
08TE63
08K0F8
08K0F8
091ZB0
096ZB0
099ZB0
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Q8K1F1
Q90529
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  4664.5
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(without alignments)
2666.544 Million cell updates/sec
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                                                                                                                                                                                                                                                                                    1 MRVPAQLLGLLLLWLPGARC...........CQVTHEGSTVEKTVAPTECS 236
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Q99m11 mus r
Q8tcj5 homo g
Q8nek1 homo s
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08wtu6
096e61
08nej1
08n355
08tbc9
08tbc9
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits, satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                            830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_barcteria:*
3: sp_fungi:*
4: sp_lunga:*
5: sp_invertebrate:*
6: sp_mammal:*
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sp_unclassified:*
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sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
sp_virus:*
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Match 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 KVTVLGQPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVET 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LLITLLAHCTGSWAQSVLAQPPSVSGAPGQIVTISCTGSSTNIGAGYAVHWYQQFPGAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 LLGLLLLMLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQLPGTAPK
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                  236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.3%; Score 977.5; DB 4; Length 236; 81.8%; Pred. No. 1.7e-77; live 20; Mismatches 21; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 TIPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 TKPSKQSNNKYAASSYLSLIPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
EMBL: BC012876; AAH12876.1; --
RMEL: BC012876; AAH12876.1; --
InterPro: IPR007110; Ig-11ke.
InterPro: IPR003006; Ig-MHC.
InterPro: IPR00306; Ig-MHC.
InterPro: IPR003596; Ig-V.
RFAM: PR0047; Ig': 2.
SMART: SM00406; IGV. 1.
RPOSITE: PS00209; IG_HIKE; 2.
RPOSITE: PS00209; IG_HIKE; 1.
RPOSITE: PS00209; IG_HIKE; 1.
RPOSITE: AS00209; IG_HIKE; 1.
RPOSITE: AS00209; IG_HIKE; 1.
RPOSITE: SS00209; IG_HIKE; 1.
RPOSITE: AS00209; IG_HIKE; 1.
                                                                                                                                                                                                                                                                                                                                                            80.5%; Score 991.5; DB 4; Length: 83.1%; Pred. No. 1e-78; Live 12; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Lung;
Strausberg R.;
Strausberg R.;
Submitted JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC030944; AAH30984.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.-11ke.
InterPro; IPR003597; Ig.-c1.
InterPro; IPR003597; Ig.-c1.
InterPro; IPR003596; Ig.-MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 83.15
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00409; IG; 2.
SM00407; IGc1; 1.
SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein
SEQUENCE 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
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      KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQ-VFGGG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
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                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                        185 TITPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 TITPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Hypothetical protein.
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla: Primates; Catarrhini; Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022099; AAH22098.1; -.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003506; Ig_MC.
InterPro; IPR003596; Ig_W.
Ffan: PF00A7; Ig' 2.
SMART; SM00406; IG'Y.
PROSITE: PS00299; IG_LIKE; 2.
PROSITE: PS00299; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 237 AA; 24884 MW; E6CF371E753968E8 CRC64;
                                                                                                                                                                                                                                                                                                      237 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Tonsil;
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δλ q δŏ 셤 ò g ğ g Strausberg R.;

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HAC OCC OS SERVING SER

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RESULT 1
App]
                                                                                                                                                                                                          (without alignments)
952.662 Million cell updates/sec
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                                                                                                                                                                            2003, 09:12:09 ; Search time 10.4815 Seconds
                                                                                                                                                                                                                                                                                                                                           1 MRVPAQLLGLLLLWLPGARC........CQVTHEGSTVEKTVAPTECS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7,
Sequence 4,
Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10,
Sequence 10,
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Sequence 1
Sequence 1
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08 487-550-10
US-09-526-098-10
US-09-372-425A-7
US-08-487-550-2
US-08-487-550-2
US-09-672A-1
US-09-672A-1
US-09-152-060-8
US-09-152-060-8
US-09-152-060-8
US-09-152-060-8
US-08-733-12
US-08-733-12
US-08-733-450-6
US-08-733-450-6
US-08-733-450-6
US-08-722-091-9
US-08-722-091-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-092-9
US-08-722-093-9
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                              using sw model
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1232
                                                                                                                           protein search,
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Match 1
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Maximum DB (
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Sequence 9, Appli Sequence 6, Appli Sequence 9, Appli Sequence 9, Appli Patent No. 5189147 Sequence 14, Appl

Sequence 3

US-09-313-942-14 US-09-025-769B-170 US-07-916-098A-56

5189147-10

Appli Appli

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Sequence 10, Application US/08487550

Patent No. 6113898

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                    9
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        Sequence Seq
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CUNTRY: USA

CIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk

COMPUTER: IEM PC compatible
ATTCREET CATCH
NUMBER: US/08/487,550
FILING DATE: 07-011-195
ATTCREETCATTON: 435
ATTCREETCATTON: 435
ATTCREETCATTON NUMBER: 012712-131
TELEPRAK: 703-836-6202
TELEPRAK: 703-836-6202
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: BURNS, DOANE, 1
699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) MOLECULE TYPE: protein US-08-487-550-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 699 Prince
CITY: Alexandria
STATE: VA
COUNTRY: USA
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     US-08-487-550-10
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66 KLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQVFGGGT 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 LLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIG-GYDLHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 LLLTLLAHCTGSWAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 236;
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 1052.5; DB 3;
; Pred. No. 4.2e-77;
10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A FILING DATE: HEREWITH CLASSIFICATION: 536 FRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: FILING DATE: ATPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 :: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                 Sequence 7, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                    Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                       Au-Young, Janice
Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.4%;
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amino acid
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Best Local Similarity 88.39
Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Cerrone, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                     Lal, Preeti
Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      Tang, Y. Tom
Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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CLONE: 2492122
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APPLICANT:
APPLICANT:
                                                                                                                                                                 US-09-049-672A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Pa
STATE: C
COUNTRY:
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                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHRNACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
FGGGTRLIVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRVPAQLLGLLLLWLPGARCESVLTQPPSVSGAPGQKVTISCTGSTSNIGGYDLHWYQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1232; DB 4; 100.0%; Pred. No. 1.7e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                           BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       RESULT 2
US-09-526-098-10
Sequence 10, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 699 Prince Street
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 236; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22314
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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 61
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Gaps

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Sequence 10, Application US/09948429B
Patent No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
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                                                                                              2, 2003, 09:18:44 ; Search time 88.5965 Seconds (without alignments) 421.442 Million cell updates/sec
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Sequence 10, A
Sequence 6, Ap
Sequence 6, Ap
Sequence 202,
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1232
1 MRVPAQLIGILILIMLPGARC..........CQVTHEGSIVEKTVAPTECS 236
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/ cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCTUG2_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
// cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                587654 seqs, 158212981 residues
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                                                                  protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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811.7
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74.4
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Perfect score:
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Sequence 96, Appl	0	88	equence 90,	equence 51,	equence 108	quence 70,	70,	70,	. ao	ω,	88	Sequence 82, Appl	equence 12,	equence 36,	equence 6,	quence 1424	0	equence 2	equence 2	Н	4	æ	7	6	e 10	5	equence 5	ednence 6	ce
US-09-972-656	US-09-972-656-1	US-09-972-656-8	US-09-972-656-9	US-09-791-153A-5	US-09-972-656-1	-09-853-161-7	-09-852-659A-7	3-852-797-	-09-853-161-88	-09-852-659A-8	US-09-852-797-8	US-10-076-747-	US-10-225-108A-	US-10-310-719-36	US-10-211-357-6	09-925-301-14	US-09-972-656	US-09-828-995B-	US-10-221-945-2	US-09-736-371	95-606-60-SD	-09-291-299A-	-09-291-299A-	-09-291-299A-	-09-291-299	US-09-988-115A-	US-09-925-664-5	US-09-796-692-9	US-10-040-862-
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ALIGNMENTS

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US/09/948,429B

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Sequence 10, Application US/10291532
Publication No. US20030180290A1
GENERAL INFORMATION:
APPLICANT: HARIARAN, KANDASAMY
APPLICANT: HANNA, NABLL
ITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
ITLLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
ITLLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
ITLLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REFERENCE: 03703/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2001-11-09
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR APPLICATION NUMBER: 09/758,173
PRIOR PELING DATE: 12091-11-09
PRIOR FILING DATE: 12091-11-09
PRIOR FILING DATE: 1999-06-07
PRIOR PELING DATE: 1999-06-07
NUMBER OF SED ID NOS: 12
SUPPLIANCE
SECTION NUMBER: 08/48',950
PRIOR FILING DATE: 1999-06-07
NUMBER OF SED ID NOS: 12.
                                                                                                                                                                                                                                                                                            61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
                                                                                                                                                                                                                                                                                                                     61 PGTAPKLLIYDINKRPSGISDRFSGSKSGTAASLAITGLQTEDEADYYCQSYDSSLNAQV 120
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                                                                                                   Length 236;
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6.6e-90;
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                                                                                              Query Match
100.0%; Score 1232;
Best Local Similarity 100.0%; Pred. No. 6.6
Matches 236; Conservative 0; Mismatches
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                            TYPE: protein
          linear
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US-10-124-807-10

US-10-124-807-10

US-10-124-807-10

SENEMATICATION NO. US20030166207A1

GENERAL INFORMATION:

APPLICANT: ANGENEON, DAIRED IR.

APPLICANT: ANGENEON: PHARMACEUTIAL. COMPOSITIONS CONTAINING, AND USE THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL. COMPOSITIONS CONTAINING, AND USE THEREOF,

TITLE OF INVENTION: IMMUNSUPPRESSANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: G99 Prince Street

CITY: ALEXANDIA

STREET: G99 Prince Street

COUNTRY: USA
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                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC_COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UUN-1995
ATTOMEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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                    INFORMATION FOR SEC ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 236 amino acids TYPE: amino acid
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703-836-2021
                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: protein
US-09-948-429B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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October 2, 2003, 13:01:50 ; Search time 3758.85 Seconds (without alignments) 15574.362 Million cell updates/sec
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1431
1 ATGAAACACCTGTGGTTCTT.......CCCTGTCTCCGGGTAAATGA 1431
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                         2888711 seqs, 20454813386 residues
                                               OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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em_htg_rod:*
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1: 9D_ba:*
2: 9D_htg:*
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5D_pat:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

em_htgo_mus:* em_htgo_other:*

em_htgo_hum:*

em_htg_mam:* em_htg_vrt:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Description			AR052282 AR052282 AR052282 AR076260 AR076260 AR076260 AR076260 AR300617 AR419496 AR419496 AR419496 AR419496 BAX419496 BAX19496 BAX19496 BAX19496 BAX19496 BAX19496 BAX19496 BAX19406 BAX1957 BAX19507 BAX	ALIGNMENTS 1431 bp DNA lin t US 6113898. 3 '' Hanna, N., Shestowsky, imatized antibodies and
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	1431 anism="unknown 462 c 385 g	40	961 CGGGAGGAGCAGTACAACAGGGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020
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QY Db	1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGTGCCAGTCCCAGATGGGTCCTGTCCCAG 60	7 A	
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Qy 24 Db 24	AACCCTCCTCAAGAGTCAACATTTCAACAGACACGTCCAAGAACAACAACAACAACAACAATCAAGAACAACAATTCAACAGAACAAGAACAAGAAACAAAAAAAA	QQ dg	GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
Qy 30	01 CTGAAGCTGAACTCTATGACCGCGGGGACACGGCCGTGTATTACTGTGTGAAA 	₹ 6 	1381 CTGCACACTACACGCAGAAGACCTCTCCCTGTCTCCGGGTAATGA 1431
Oy 36	361 CTTTTTCAGTTGTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420 	AR	1431 bp
Oy 42 Db 42	421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480 	W C A D	Sequence 11 from patent AR265201 AR265201.1 GI:29693622
Oy 48	481 TCCAAGAGCACCTCTGGGGGCACAGGGGCCTGGCTGCCTGGTCAAGGACTACTTCCCC 540 	S R	_
Oy 54. Db 54.	541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 600 		AUTHORS Aquin, S. and Vezina, Louis. P. TITLE Method for producing polyhydroxyalkanoates in recombinant organisms JOHNAL Patent: US 6492134-A 11 10-DEC-2002; FEATURES Location/Qualifiers
Qy 6(601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660 	BA	SOUTCE
QY 6(661 AGCTTGGGCAGCCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTG 720 		Query Match Best Local Similarity 100.0%; Score 1431; DB 6; Length 1431; Best Local Similarity 100.0%; Pred. No. 6.2e-277; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 72: Db 72:	21 GACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACGTGCCCACGTGCCCAGCA 780 	da da	1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAAATGGGTCCTGTCCCAG 60
Qy 78	81 CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC 840 	୍ଷ ବର୍ଷ ବର୍ଷ	61 GIGCAGCIGCAGGAGICGGGCCCAGGACIGGIGAAGCCIICGGAGACCCIGICCCICACC 120
Oy 8,	41 ATGATCTCCGGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCCT 900 	δ g	121 TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCC 180
96 4g	01 GAGGTCAAGTTCAACTGGTACGTGGACGCGTGGAGGTGCATAATGCCAAGACAAAGCCG 960 	δδ ; 	181 CCAGGAAGGGCTGGAGTGGAATTGGGAGTTTCTATAGTAGTAGTGGGAACACCTACTAC 240

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SUMMARIES		AAT62513	AAV35489	AAS17247	AAT62510	AAV35485	AAS17243	AAC66522	AAT18059	
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% Query Match		100.0	100.0	100.0	91.9	91.9	91.9	89.2	88.1	
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ALIGNMENTS

AAT62513 standard; DNA; 1431 BP.

RESULT 1

25-MAY-1997

AAT62513;

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Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
                                                                                         Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic luqua erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
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Chimeric Homo sapiens.
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Shestowsky WS;

Brams P, Hanna N,

Anderson DR,

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                                                                                                                                     2 DNA sequences (AAT62512 and AAT62513) respectively code for primatised forms (AAW01821 and AAW01822) of the light and heavy chain of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody into an expression vector (pref. NEOSPLA) which contains human light and heavy to an constant region genes to allow prodm. of primatised antibody in e.g. CHO cells. Primatised 7010 and 736 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                             B7.1 or B7.2 antigen r graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1431; DB 18; Length Best Local Similarity 100.0%; Pred. No. 6.3e-286; Matches 1431; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                             human B
                                                           antibody binding huma
19 autoimmune disease
                                                                                                         Claim 11; Fig 10B; 81pp; English
            1997-108638/10.
                                                                           treating
                                                           monoclonal
                            P-PSDB; AAW01822
                                                                           for
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BX439438 BU146962 RX415818 BX415883 BX415883 BX415883 BX41581 BX41581 BX41592 BX41592 BX41592 BX41592 BX41592 BX41592 BX41592 EXAMO7892 EXAMO7892

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BX457369

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AGENCOURT BX456326 BX388631

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BX367600

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BQ711727 BQ705928

BX432300

BX397632 BX339318 BX380759

BX339318 BX380759

BX378450 BX408117 BX396322

BX378450 BX408117 BX396322

BX378450

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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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REFERENCE AUTHORS TITLE JOURNAL COMMENT Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES £ Query Match Length DB

BX377695 BX377695 BX414495 BX414495 BQ062878 AGENCOURT BX337477 BX337477

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13 13 13

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66.0 65.0 63.0 62.8

944 929.6 902 899.2

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Score

NO. Result

Entarryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Livw B., Gruber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Longublished

Contact: Genoscope

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefégenoscope.ons.fr. Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 7198.r For

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0D1009E0SNP1scluster=7198.r. Contact:

Feng Liang Email: fliangdlifetech:com URL:

Feng Liang Email: fliangdlifetech:com (Corporation 1600) BX377695 1201 bp mRNA linear EST 08-MAY-2003 38737695 HOMO Sapiens PLACENTA COT 25-NORMALIZED HOMO Saplens CDNA CLONE CSDI009YJ10 3-PRIME, mRNA sequence. BX377695.1 GI:30439018 Homo sapiens (human) Homo sapiens

224

164

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Contact: Genoscope
Contact: Genoscope
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198 r. For
more information about this cluster, see
http://www.genoscope.cns.fr
cgi.bin/cluster.cgi/seq-c500Ap001AE07NP1&cluster=7198 r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fullength.livitrogen.com/ InvitroGen Corporation 1600
Faraddy Avenue Genoscope sequence ID : C50CAP001AE07NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib_"Homo sapiens THYMUS"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
20 others
21 290 21 251 27 others
                                                                                                                                                                                 1358 CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGGCCTCTCCCTGT 1417
                                                                                                                                                                                                                                                                                                                                                               mRNA linear EST 13-MAY-2003 sapiens cDNA clone CSOCAPO01Y113
                                                                                                                  1298 TCTTCCTCACAGCAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCT 1357
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                                                                                                                                                                                                  Euteleostomi;
   283 AIGGGCAGCGGGAGAACAACTACAAGACCACGCTCCCKTGCTGGACTCCGACGGCTCCT
                                                                                                                                    463 TTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGGGGCCACAGCGGCCCTGGGGCTGCCTG
                                                    1238 ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGGTGCTGGACTCCGACGGCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 1142)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full.Length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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4114495 Homo sapiens THYMUS Homo
3-PRIME, mRNA sequence.
BX414495
BX414495,1 GI:30637021
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Matches 952; Conserv
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AUTHORS
TITLE
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
296 c 396 g 267 t 54 others
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Faraday Avenue Genoscope sequence ID : CSODI009DE05NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                             Length 1201;
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Pred. No. 4e-215;
; Mismatches 22;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                           17;
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95.8%;
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Page 1

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN BY.1 AND/OR BY.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN GUPPRESANTS"

TITLE OF INVENTION: IMMUNSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                             APPLI
                                                                                                                                                                                                                                                          Sequence 2, A
Sequence 68,
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
               US-09-343-485A-3
US-08-487-550-7
US-08-157-101A-6
US-08-157-101A-6
US-08-157-101A-9
US-08-157-101A-9
US-08-147-101A-9
US-08-147-275-2
US-08-475-815B-3
US-08-475-815B-3
US-08-475-815B-3
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US-09-023-715-2
US-09-025-986-08
US-09-025-985-68
US-09-121-952A-68
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Patent No. 6113898
GENERAL INFORMATION:
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/COCKET UNMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEFONE: 703-836-6620
TELEFAX: 703-836-6201
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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- 2003 Compugen Ltd.
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US-09-04-05-058-3

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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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	Description	Sequence 11. Appl	Sequence 11, Appl	Sequence 11. Appl	Sequence 11. Appl	Sequence 6. Appli	'n	Segmence 3. Appli	m	, ~	Sequence 2, Appli		=	i ,	_		
SUMMARIES	ID	US-09-948-429B-11	US-10-124-807-11	US-10-291-532-11	US-10-124-905-11	US-10-073-138-6	US-09-948-429B-3	US-10-124-807-3	US-10-291-532-3	US-10-124-905-3	US-10-073-138-2	US-10-211-357-7	US-10-211-357-11	US-10-211-357-9	US-10-203-754A-40	US-09-740-002-17	US-10-225-108A-1
	DB	10	12	12	13	13	10	12	12	13	13	14	14	14	12	σ	13
	% Query Match Length DB	1431	1431	1431	1431	1431	1431	1431	1431	1431	1431	1404	1404	1404	1428	1428	1430
	& Query Match	100.0	100.0	100.0	100.0	99.	91.9	91.9	91.9	91.9	91.8	82,5	82.3	82.2	80.4	79.3	79.2
	Score	1431	1431	1431	1431	1429.4	1315.8	1315,8	1315.8	1315.8	1314.2	1181	1177.8	1176.2	1151	1134.8	1134
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US-09-848-832-1	US-09-925-299-230	3-09-92	<u>_</u>	US-09-954-456-789	US-09-954-456-1604	US-09-87	08-60-sn	US-09-87	US-10-22	US-09-747-66	US-09-747-669-2	703	20	1-948-42	-80)-291	US-10-124-905-7	US-10-073-138-4	US-10-066-895-20	US-10-066-895-25	US-10-066-895-27	US-10-150-475A-7	US-10-066-895-14	US-09-822-698A-27	US-09-822-849A-87	US-09-822-830A-571	US-09-911-692-3	US-09-911-703-3
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79.2	79.2	79.2	78.6	78.5	78.5	78.5	78.5	78.5	78.1	78.1	78.1	78.1	78.1	77.7	77.7	77.7	77.7	77.7	77.6	-	77.5	77.2		76.9	٠.	٠.	9.92	
1134	1133.4	1133.4	1125.2	1122.8	1122.8	1122.8	1122.8	1122.8	1118	1118	1118	1118	7	1112.4	1112.4	1112.4	1112.4	1112.4	1110.8	1110.8	1109.2	1104.8	1102.8	1100.4	\circ		1096.6	1096.6
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ALIGNMENTS

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Sequence II, Application US/09948429B
Patent NO. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION:
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE ADDRESS:
ADDRESSEE: BORNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
OPERATING SYGTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
FILING DATE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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US-09-948-429B-11
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Db 781 CCTGAACTCCTGGGGGACCGTCAGTCTTCCCCCCAAAACCCAAGGACACCCTC 840 Qy 841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGACGTGAGCCACGAAGACCT 900	Qy 1021 GACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAGCCTCCCAGCCCC 1080	1081 ATCGAGAAAACCATCTCCAAAGGCCAGGGCCCGAGAACCAGGGTCAGCCTG 1141 CCCCCATCCCGGGATGAGCCTAACCAGGTCAGCCTG 1141 CCCCCATCCCGGGATGAGCTGACCAGGGTCAGCCTGAGCGTGAGCGTGAGCTGCTG 1141 CCCCCATCCCGGGATGAGCTGACCAGAGAGCTGGTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGGGCTGAGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGAGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGAGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGGCTGAGGAGCTGAGGGCTGAGGAGCTGAGGGCTGAGGAGGGCTGAGGAGGCTGAGGAGGAGGGCTGAGGAGGAGGGCTGAGGAGGAGGAGGAGGAGGAGGGAG	1201	Qy 1261 AAGACCACGCTCCCGTGCTGGACTCCGACGCTCCTTCTTCCTCTACAGCAAGCTCACC 1320	QY 1321 GTGGACAAGAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380 DD 1321 GTGGACAAGAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCT 1380	OY 1381 CIGCACAACCACTACACGCAGAAGAGCCICICCCCGGGTAAATGA 1431	RESULT 2 US-10-124-807-11 ; Sequence 11, Application US/10124807	on No. US20030166207A1 INFORMATION: ANT: Anderson, Darrell R. OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC	; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS; TITLE OF INVENTION: IMMUNOSUPPRESANTS" ; NUMBER OF SEQUENCES: 12	; CORRESPONDENCE ADDRESS: ; ADDRESSE: BURNS, DOANE, SWECKER & MATHIS ; STREET: 699 Prince Street ; CITY: Alexandria	; STATE: VA ; COUNTY: USA ; ZIP: 22114 ; COMPUTER READABLE FORM:	<pre>// MEDIUM TYPE: Floppy disk // COMPUTER: IBM PC compatible // OPERATING SYSTEM: PC-DOS/MS-DOS // SOFTWARE: PatentIn Release #1.0, Version #1.30</pre>	; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/10/124,807 ; FILING DATE: ; CLASSIFICATION:	; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: 09/383,916 ; FILING DATE:
INFORMATION FOR SEO ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1431 base pairs TYPE: nucleic acid STRANDEDDESS: not relevant TOPOLOGY: incar MOLECULE TYPE: peptide FRANURE: RAMF(KEY: CDS LOCATION: 11431 FRATURE: NAME/KEY: mat_peptide US-09-948-429B-11 US-09-948-429B-11	Query Matc Best Local Matches 14	QY ATGRACACTGTGTTCTTCTCTGTGGCAGCTCCCAGATGGGTCCTGTCCCAG		OY 181 CCAGGGAAGGGGCTGGAGTGGATTGGGGGTAGTAGTAGTGGGAACACCTACTAC 240 	QY 241 AACCCTCCTCAAGAGTCAAGTCACCATTTCAACAGACAGCTCCAAGAACGGTTCTCC 300 14111111111111111111111111111111111	E - E	Qy 361 CTTTTTCAGTTGTAGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC 420	QY 421 CTGGTCACCGTCTCTCAGGTAGCACGCCCATCGGTCTTCCCCCTGGCACCCTC 480	Oy 481 TCCAAGAGCACCTCTGGGGGCACAGGGCCTGGGCTGGTCAAGGACTACTTCCC 540	QY 541 GAACCGGTGACGGTGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 600 	OY 601 GCTGTCCTACAGTCCTCAGACTCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660	OY 651 AGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCGAGCAACAAGTG 720- 	QY 721 GACAAGAAAGCAGAGCCAAATCTTGTGACAAAACTCACAATGCCCACGTGCCCAGCA 780	OY 781 CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCTC 840

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October 2, 2003, 08:56:23 ; Search time 55.856 Seconds (without alignments) 1352.654 Million cell updates/sec
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2549
1 MKHIWFFLLLVAAPRWVLSQ.......MHEALHNHYTQKSLSLSPGK 476
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Primatised anti-bu	Macaque primatized	Protein segmence	Human immine syste	Primatised anti-hu	Macagine primarized	Protein seguence	Monoclonal antibod	Human immune syste
SUMMARIES B ID	18 AAW01822	19 AAW63765	23 AAU11646	22 AAB36206	18 AAW01818	19 AAW63761	23 AAU11539	17 AAR93553	21 AAY44721
% Query Ratch Length DB	476							475	
% Query Match	100.0	100.0	100.0	91.9	90.6	90.6	90.6	90.1	89.4
Score	2549	2549	2549	2342.5	2309	2309	2309	2296.5	2278
Result No.	н	63	m	4	ហ	φ	7	80	6

Anti-rhesus D reco 4A5-3.1.1-B4 antib Reshaped CD4 antib Human gamma-4 PE he Human gamma-4 PE he Human gamma-4 E hea Ganglioside GD2 sp Human anti-RSV mon Antino acid sequenc Human E27 anti-IgE Mus musculus anti- Antino acid sequenc E27 anti-IgE antib Full length heavy Wus musculus anti- Mus musculus anti- Hught chain amino Anti-IgE antibody, Full length heavy Full length heavy Human RSV antibody Human RSV antibody Respiratory syncyt Human immunoglobul Human immunoglobul Human immunoglobul Humanised high pot	6C10 heavy chain. ue; 16C10; suppressive; hia purpura; ritis; psoriasis; isease;
17 AAR93166 24 ABP96396 13 AAR22759 13 AAR22756 13 AAR22756 13 AAR14925 16 AAW14925 17 AAW05829 17 AAW1639 22 AAW1639 22 AAW1639 20 AAW95663 21 AAW1639 22 AAW95663 22 AAW95663 22 AAW95661 22 AAW95661 22 AAW95661 22 AAW95661 22 AAW95661 23 AAW95661 24 AAW95661 22 AAW95661 22 AAW95661 23 AAW95661 24 AAW95661 25 AAW95661 26 AAW95661 27 AAW95661 28 AAW96661 29 AAW9661 20 AAW9661 21 AAW9661 22 AAW169467 23 AAW9661 24 ABU69467 24 ABU69467 25 AAW169467 26 AAW169467 27 AAW169467 28 AAW169467 28 AAW169467 29 AAW169467 20 AAW169467 21 AAW169467 22 AAW169433 24 AAW169433 25 AAW169433 26 AAW169433 27 AAW169433 28 AAW169433 28 AAW169433 28 AAW169433	n; 476 AA. n; 476 AA. l antigen antibody i molgus monkey; macaq ntigen; CDS9; immuno athic thrombocytopae sus; rheumatoid arth graft versus host d ctoma. s; s; s;
88 88 88 88 88 88 88 88 88 88 88 88 88	standard; Protein; 97 (first entry) d anti-human B7.1 l antibody; B7 ante d disease; diopat antibody; B7 ante d disease; idiopat bridoma; transfect bridoma; transfer brido
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cell proliferation.

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2 Polypeptides (AAW01821 and AAW01822) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 16610. Cloned 16610 light and heavy variable genes (see also AAT62512 and AAT62513) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. GHO cells. Primatised 7C10 and 7B6 anti-B7.1 antibodies have also been produced (see also AAW01817-20). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                        ·,
                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 2549; DB 18; Length 476; 100.0%; Pred. No. 5.8e-149; O; Mismatches 0; Indels 0;
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                                                                                               Claim 14; Fig 10B; 81pp; English.
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                                                                                                                                                                                                                                                                                                     and graft-versus-host disease
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 1997-108638/10.
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WPI; 1997-100050,
N-PSDB; AAT62513
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This sequence represents a primatized form of the antibody 16C10 heavy chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell? B cell interactions, particularly autoinmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression and antigen-specific immunosuppression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                                                                                                                                                                New monoclonal antibodies specific for B7.1 or B7.2 antigens and mibiling binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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100.0%; Pred. No. 5.8e-149;
tive 0; Mismatches 0;
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nes 476; Conservative
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                                    Macaca fascicularis
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                                                                       WO9819706-A1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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October 2, 2003, 08:56:23 ; Search time 13.1295 Seconds (without alignments) 1704.917 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-758-173-12 2549 1 MKHIWFFILLIVAAPRWVLSO.......MHEALHNHYTQKSLSLSPGK 476

127863 seqs, 47026705 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	57 homo	59 homo sap	51 homo	70 oryct	52 cavia	50 homo s	13	P20761 rattus norv	Som som 83	snw 98	snm 69	P03987 mus musculu	P01863 mus musculu	54 mus	55 mus	7	20	som som 95	57 mus	54 homo	55 rattu	'n	l homo	l homo	988 oryct	^-	ory	~	mus mu	homo		mesoc	04220 homo sa
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ALIGNMENTS

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                                                                                                                                                                                                                                                                  "Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9 - and 2.8 A resolution.";
Biochemistry 20:2361-2370/1981).
-!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3) MARKER & THE GIM (NON-1) MARKERS IN THE AMIDATION STATES OF 35.116,198.269 & 272.
-!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF 268-272.
                                                                                       Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal
1gd1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003623; F:antigen binding activity; TAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0037110; Ig-1ike.
InterPro; IPR003507; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SWART; SMO407; IGC1; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
MEDLINE=81208100; PubMed=7236608;
Deisenhofer J.;
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HINGE.
CH2.
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                                                    DISULFIDE BONDS.
MEDLINE-77070267; PubMed-1002129;
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
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PDB; 1D5B; 09-FEB-00.
PDB; 1D5B; 09-FEB-00.
PDB; 1D5V; 09-FEB-00.
PDB; 1DN2; 17-MAY-00.
PDB; 1DN2; 17-MAY-00.
PDB; 1EAK; 06-JUL-95.
PDB; 1EXC; 20-JUL-95.
PDB; 11X; 16-MAY-01.
PDB; 12X; 16-MAY-01.
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Q96kx8 homo
Q96bb9 homo
Q8wukl homo
Q99m22 mus n
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Q96ga6 homo s
Q8my24 homo s
Q91wp5 mus m
Q91wr1 mus m
Q99xa4 mus m
Q91z07 mus m
Q91z07 mus m
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Q8k172 mus n
Q8k0f2 mus n
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Q8vea0 mus n
Q8k0z4 mus n
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Q96dk0 homo
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Q96k68 hc
Q91x92 r
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85.2%; Pred. No. 9.9e-162;
ive 16; Mismatches 45; Indels 9;
                                                                                                                                                            Q8vcx7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Straubberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -.
R InterPro; IPR007106; Ig-MFC.
R InterPro; IPR003596; Ig-W.
R Pfam; PF0047; Ig: 4.
R SMART; SM00406; IG-X, IG-IKE; 4.
R PROSITE; PS00290; IG-MHC; 2.
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SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
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Q95K68
Q91X92
QBNCL6
Q96GA6
Q96GA6
Q91WA1
Q991WP5
Q91LW7
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096BB9
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les 403; Conserv
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Matches
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    28TC77
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Q991c4 mus musculu
Q96141 mus musculu
Q971a4 mus musculu
Q971a1 mus musculu
Q99131 mus musculu
Q99135 mus musculu
Q8r3h6 mus musculu
Q8r3h6 mus musculu
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Q95m34 equus cabal
Q96ey0 homo sapien
Q9bu10 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapien
sapien
                                                                                                                                                "Search time 46.0645 Seconds (without alignments) 2666.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                             2549
1 MKHLWFFLLLVAAPRWVLSQ.......MHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8tc63 homo se O8tc63 homo se O8n4y9 homo se
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Q8n4y9 homo s
Q8nf17 homo s
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                     5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                               830525 seqs, 258052604 residues
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                     GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                2003, 08:56:23 ;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          protein search, using sw model
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QBTC77
QBNF17
Q99LC4
Q9BLC4
Q9B124
Q9P131
Q99L35
Q9P125
Q9F125
Q9F126
Q9
                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_virus:*
sp_vertebrate:*
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sp_phage:*
sp_plant:*
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sp_bacteriap:*
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Maximum DB seq length: 200000000
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Match Length
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146927
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PEVQENWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTYLHOODWLNGKEYKCKVSNKGLPS 356
                                                                       240 VDKRVESK---YGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED 296
                                                                                                              PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 359
                                                                                                                                                                                    PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WYGCFRSKAHKSTIEYAASVKGRFTILRDDSKNSVHLQMNSLKTDDTAVYYCVRD--LEG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 VGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 ELKTPLGDTTHTCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 WIGSFYSSS--GNTYYNPSLKSQVIISTDISKNQFSLKLNSMTAADTAVYYCVRDRLFSV 124
                                                                                                                                                                                                                                                            476
                                                                                                                                                                                                         SIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN
                                        VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 WVLLVVFLQGVQCEVQLVDSGGGLVQPGGSLRLSCAASGFIVSDHY-VEWVRQAPGKGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 FLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQPPGKGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---EPKSCDKTHTCPP
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                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178; AAH33178.1; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2AC7D22E72D6CAA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 75.6%; Score 1927.5; DB 4; Local Similarity 72.4%; Pred. No. 1.6e-147; Hes 376; Conservative 32; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                      521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Primary B-Cells from Tonsils;
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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SWART; SM00407; 16c1; 3.
SWART; SM00406; 16c1; 3.
PROSITE; PS50835; 1G_LIKE; 4
PROSITE; PS00290; 1G_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                         22,
23,
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01-OCT-2003 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 2:
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE 521 AA;
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                                                                         243
                                                                                                                                               303
                                                                                                                                                                  239 VEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 298
                                                                                                                                                                                                                     363
                                                                                                                                                                                                                                                                                                            TISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 PPGKGLEWIGTI-NFSGNMYYSPSLKSRVTWSADMSENSFYLKLDSVTAADTAVYYCAAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 RLFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 PPGKGLEWIGSFYSSSGNTYYNPSLKSQVTISTDTSKNOFSLKLNSMTAADTAVYYCVRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PEPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSI-SGGYGWGWIRQ 59
VGMVYNNW-FDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                     179 TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK
                                                                                                                                                                                                                   FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                       TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKK
                                                                                                                                           244 AEPKSCDKTHICPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                          299 FNWYVDGVEVENEAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                               PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                      419 PPVLDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMHEALHNHYTQKSLSLSPGK 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Kidney,
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025895; AAH25885.1; -.
InterPro; IPR001923; BlueCu_1.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR00306; Ig_W.
Pfam; PF00047; ig; 4.
SMART; SM00406; iGv; i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E29920B09BA369F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.4%; Score 2075; DB 4;
83.2%; Pred. No. 1.7e-159;
1ve 29; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
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Mammalia; Eutheria; Primates;
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Best Local Similarity 83.29
Matches 397; Conservative
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SEQUENCE 4
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October 2, 2003, 09:12:09; Search time 21.1407 Seconds (without alignments) 952.662 Million cell updates/sec
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2549
1 MKHLWFFLLLVAAPRWVLSQ..........MHEALHNHYTQKSLSLSPGK 476
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                      328717 seqs, 42310858 residues
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                    Run on:
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

328717

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Issued_Patents_AA:* Database :

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		12	4	equence 4,	equence 4,	ω,		12,	œ	10,	18	18	ď	ď	78	equence 2,	7	equence 14,	equence 16,	65,	14,	•	14,	16,	e 25,	equence 27,	œ
f	TD	-487-55	-09	-09-049-672A	-08-4	-526-09	-08-793-45	-08-397-411-	-894-	-08-523-	-08-523-	-08-887-	S-09-109-	-09-282-505-	-09-024-	-09-296-005-	-09-282-846-	-09-680-145-	8-08-887-3	-08-887-352	S-08-466-1	S-09-109-2	-09-109-	-09-296-005-1	-09-296-	S-09-740-002-2	S-09-740-002-2	-08-466-151-
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S Query	March				90.6							٠.	83.4	83.4	83.4	83.4			83.3		83.3						82.2	82.1
9	arose	2549	2549	2342.5	2309	2309	2200	2153.5	2145.5	2144.5	2137.5	2126	2126	2126	2126	2126	2126	2126	2124	2124	2124	12	12	12	212	Ċ.	2094.5	60
Result		1	7	m	4	S	9	7	80	on :	10		12		14	15	16	17	18	19	20	21	22	23	24	25	26	27

Sequence 8, Appli	Sequence 71. Appl		Sequence 71, Appl	•		Sequence 2, Appli	Sequence 2, Appli	'n	Sequence 7, Appli	8,	Sequence 8, Appli	Sequence 13, Appl	ω	22,	22,	Sequence 22, Appl
US-08-466-163B-8	US-09-027-449-71	US-09-026-985-71	US-09-121-952A-71	US-09-234-340A-71	US-08-378-939-10	US-09-679-397-2	US-09-680-148-2	US-09-304-465A-2	US-08-157-101A-7	US-08-487-550-8	US-09-526-098-8	US-08-458-516-13	US-09-049-672A-8	US-07-934-373C-22	US-08-437-642B-22	US-08-146-206C-22
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453	452	452	452	452	476	449	449	449	459	478	478	449	467	454	454	454
82.1	81.3	81.3	81.3	81.3	80.9	90.8	80.6	9.08	80.6	80.5	80.5	79.8	79.4	79.1	79.1	79.1
2093	2071.5	2071.5	2071.5	2071.5	2063	2053.5	2053.5	2053.5	2053.5	2053	2053	2033	2024.5	2016.5	2016.5	2016.5
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ALIGNMENTS

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
THE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
ADDRESSE: BUTNES, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: TEEKTAIN NUMBER: 35,030
REFERENCE/POCKET UNBER: 35,030
REFERENCE/POCKET UNBER: 012712-131
TELECOMMULCATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 2549; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.5e-198;
Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk

AMDIUM TYPE: Floppy disk

                                                                                                                        ; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              703-836-2021
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RESULT 1
US-08-487-550-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
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                                                                                                                                                    1 MKHIWFFLLLVAAPRWVLSQVQLQESGPGLVKPSETLSLTCAVSGGSISGGYGWGWIRQP 60
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                                                                                             Gaps
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                                                        Length 476;
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APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Ociley, Neil C.
APPLICANT: Guegler, Kail J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                           Indels
                                                        Query Match 100.0%; Score 2549; DB 4; Best Local Similarity 100.0%; Pred. No. 1.5e-198; Matches 476; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEXED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillman, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
   protein
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 ; MOLECULE TYPE:
US-09-526-098-12
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APPLICANT:
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                                                                                             Sequence 12, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONNEX MONCCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "MONNEX MONCCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THER TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
PGKGLEWIGSFYSSSGNTYYNPSLKSQVIISTDISKNQFSLKLNSMTAADIAVYYCVRDR
                   LFSVVGMVYNNWFDVWGPGVLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
                                                                                                                                              EPVIVSWNSGALISGVHIFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP
                                                                                                                                                                                                                                                                                                                                                                   IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY
                                                                                                                                                                                                                                                                                                                                                                                         KTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin RC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILIG DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 476 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-526-098-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
TOPOLOGY:
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61
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October 2, 2003, 09:18:44; Search time 178.695 Seconds (without alignments) 421.442 Million cell updates/sec
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2549
1 MKHIWFFLLLLVAAPRWVLSQ..........MHEALHNHYTQKSLSLSPGK 476
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            Perfect score:
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                                                                       OM protein
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

587654 seqs, 158212981 residues

Searched:

Published_Applications_AA:* Database :

/cgn2_f/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/cgn2_f/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_f/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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Cgn2_6/ptodata/2/pubpaa/USG0_EVBCOMB.pep.*
Cgn2_6/ptodata/2/pubpaa/USG10_EVBCOMB.pep.*
Cgn2_6/ptodata/2/pubpaa/USG10_EVBCOMB.pep.*
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Cgn2_6/ptodata/2/pubpaa/USG0_EVBCOMB.pep.*
Cgn2_6/ptodata/2/pubpaa/USG0_EVBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 12. Appl	1:	1	2 5	1	` ~	Sections 4. Applia	. 4	Sequence 1, Appril	Sequence 8 annul	Segmence 37 april	Sequence 10 April	Sequence 66. Appl	Sequence 18 April	Sequence 18, Appl
qı	US-09-948-429B-12	US-10-124-807-12	US-10-291-532-12	US-10-124-905-12	US-09-948-429B-4	US-10-124-807-4	US-10-291-532-4	US-10-124-905-4	US-10-211-357-12	US-10-211-357-8	US-10-310-719-37	US-10-211-357-10	US-09-925-179-66	US-09-920-171-18	US-10-113-996-18
DB	101	12	12	14	10	12	12	7	12	12	12	15	Η	σ	12
Length	476	476	476	476	476	476	476	476	467	467	580	467	451	451	451
Query Match Length DB ID	100.0	100.0	100.0	100.0	90.6	90.6	90.6	90.6	84.2	84.1	83.9	83.9	83.4	83.4	83.4
Score		2549	2549	2549	2309	2309	2309	2309	2145.5	2144.5	2138	2137.5	2127	2126	2126
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Sequence 2, Appli Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl Sequence 65, Appl	43, 218, 25,	250, 25, Ag 68, Ag 216, Ag	4 , , , 0, 0, 0, 0, 0	Sequence 37, Appl Sequence 220, App Sequence 220, App Sequence 45, Appl Sequence 226, App Sequence 254, App Sequence 254, App
US-10-292-869-2 US-09-792-938-2 US-09-920-171-14 US-09-925-171-16 US-09-925-179-6	12 US-10.113-996-14 12 US-10-113-996-16 9 US-09-796-848A-43 10 US-09-996-288-218 10 US-09-996-288-250 11 US-09-996-288-250	US-09-996-265-251 US-09-740-002-25 US-09-925-179-68 US-09-996-288-49	US-09-796-8488-41 US-09-796-8488-41 US-09-996-288-222 US-09-996-265-222	- 28 88 - 2 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88 88 - 2 88
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ALIGNMENTS

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Sequence 12, Application US/09948429B
Patent No. US20020177689a1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PARAMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/487,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-09-948-429B-12
                                                                                                                                                                                                                                                                                                                                                             STATE: V
COUNTRY:
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PGKGLEWIGSFYSSGNTYYNPSLKSQVTISTDTSKNQFSLKLNSMTAADTAVYYCVRDR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HANNA, NABIL
TITLE OF INVENTION: ANTI-COBO ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: ANTI-COBO ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REPERBENCE: 037003/291872
CURRENT APPLICATION NUMBER: US/10/291,532
CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 60/331,187
PRIOR PILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR PLING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KITPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2549; DB 12;
100.0%; Pred. No. 1.1e-172;
iive 0; Mismatches 0;
                                                                                                                                                             012712-131
                                                       UMBER: US 08/487,550
07-JUN-1995
                          09/383,916
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Sequence 12, Application US/10291532

Publication No. US20030180290A1

GENERAL INFORMATION:

APPLICANT: HARIHARAN, KANDASAWY

APPLICANT: HANNA, NABIL
                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                           35,030
                                        FILING DATE:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
RAME: TESKIN, ROBIN I.
REGISTRATION NUMBER: 35,03
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-10-124-807-12
        PRIOR APPLICATION DATA:
                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 linear
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Best Local Similarity
Matches 476; Conserv
                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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Publication No. US20030166207A1
Publication No. US20030166207A1
Publication No. US20030166207A1
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONEXY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: IMANOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOURCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSOURCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                           Length 476;
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                                                                                                                                                                       100.0%; Score 2549; DB 10;
100.0%; Pred. No. 1.1e-172;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRNIT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: UNINS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                          Best Local Similarity 100.
Matches 476; Conservative
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                              MOLECULE TYPE: protein US-09-948-429B-12
                                                                             TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ITCTCTGGCTCCAAATCAGGGAACACCCCCACCCTGACCATCAACGGGGTCGAGGCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACCIGIGGGGAGACAACAGIAGAAAIGAAIAIGICCACIGGIACCAGCAGAAGCCAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCCCCTATACTGGTCATCTATGATGATGACGGCCCCTCAGGGATCCCTGAGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 705; DB 4; I Best Local Similarity 100.0%; Pred. No. 3.7e-186; Matches 705; Conservative 0; Mismatches 0;
                        Version #1.30
                                                                                                                                                                                       NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                            APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                    US/09/526,098
                     Release #1.0,
        PC-DOS/MS-DOS
                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
                                                                                                                                                                                                                                                                                                             : 705 base pairs
nucleic acid
EDNESS: not relevant
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
      OPERATING SYSTEM: PC-I
SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                    APPLICATION NUMBER:
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                                                                   FILING DATE
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US-09-526-098-1
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
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Mismatches 0;
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ADDRESSE: BURNS, DOAND, SWECKER & MATHIS STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09526098 Patent No. 6492134 GENERAL INFORMATION:
Best Local Similarity 100.0%; P
Matches 705; Conservative 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Sequence 1, Application US/08487550 Patent No. 6113898
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NAME: Teskin Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Alexandria
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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FEATURE:
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FEATURE:
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STATE: V
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US-08-487-550-1
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Sequence 62, Appl
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Sequence 5, A
Sequence 9, A
Sequence 9, A
Sequence 20,
Sequence 11,
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Sequence 29,
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Sequence 23
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     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-702-705-1625
US-09-736-457-1625
US-09-592-998C-7
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US-09-526-098-1

US-08-487-550-9

US-09-526-098-9

US-09-526-098-9

US-09-378-939-11

US-09-049-672h-25

US-09-049-672h-25

US-09-049-672h-25

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US-09-1620-312-62
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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE 3.12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
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OPERATOR SOFTWARE: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-Bos/MS-DOS
SOFTWARE: Patentin Pc-Bos/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                            US-09-338-933-268
US-09-215-681-268
US-09-702-705-1589
US-09-736-457-1589
US-09-736-457-409
US-08-97-894-419
US-09-588-281-241
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/note="Corgan: Spleen: Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dr priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Supersoript II RT (Life Technologies). Note: this is a
NHL MGC Library.

NHL MGC Library.

17 a 284 c 245 g 174 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 GAAACAATATTGGAAGTAAAAAGTGTGCACTGGTACCAGGAGAGGCCAGGCCAGGCCCGTG 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGACTCAGCCACCCTCGGTGTCAGTGTCCCCAGGACAGACGGCCAGGATCACCTGTGGGG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACTCAGCCACCCTCGGTGTCAGTGGCCCCAGGACGACGACAATTACCTGTGTGG 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGACAACAGTAGAAATGAATATGTCCACTGGTACCAGCAGAAGCCAGGGGGGGCCCCTA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAAATCAGGGAACACCCCCACCCTGACCATCAACGGGGTCGAGGCCGGGGATGAGGCTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Matson
cDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2474 row: 1 column: 21
High quality sequence stop: 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGCCTATGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGTTCTCCTCCGCCTCCTCTCACTG - - - CACAGGCTCTGTGACCTCCTATGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGATTCTCTGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATC---CGGTCTTCGGAGGAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGGGTGACCGTCCTAGGTCAGCCCAAGGCTGCCCCTCGGTCACTCTGTTCCCGCCCT
                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 931)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.8%; Score 555.6; DB 13; Length 931;
larity 89.3%; Pred. No. 1.7e-125;
Conservative 0; Mismatches 69; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 623; Conserv
      BQ709526
BQ709526.1
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                          /lab_host="Delion (proper resistant)"
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/note="Corgan: Splean; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCACGAG(GG). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
1282 c. 254 g. 173 t. 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGCCCCTATACTGGTCATCTATGATGATGACCGGCCCTCAGGGATCCCTGAGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 TCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302 ATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGATCATCCGGTCTTCGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 TCTACCCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCCGTCAAGGCGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              542 IGGAGACCACCACACCCTCCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCTACCTGA
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                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                    Score 558.8; DB 13
Pred. No. 2.8e-126;
); Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ709526 931 bp
AGENCOURT_8443486 NIH_MGC_113 Homo
5', mRNA sequence.
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/clone="IMAGE:6279618"
location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                    79.3%;
ilarity 91.9%;
Conservative
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333 367 427 453

DEFINITION RESULT 2 BQ709526

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

E I (bases 1 to 952)

E I (bases 1 to 952)

I (bases 1 to 952)

I (published

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-rémail.nih.gov

Tissue Procurement: Dr. Mark Watson

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LCM2469 row: h column: 19

High quality sequence stop: 584.
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BQ711447

BG711447

BG711447.1 GI:21850346
    BQ707953 AGENCOURT
BQ712246 AGENCOURT
BQ712246 AGENCOURT
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BC776411 GO2709539
BC776411 GCZ709539
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    BQ707953
BQ708246
BQ710672
BQ746204
BQ8746204
BQ746205
BQ726256
BQ72626
BQ709509
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BQ709509
BQ75301
BG75501
BG775501
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Homo sapiens
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1 ATGAGGGTCCCCGCTCAGGT......CCCCTACAGAATGTTCATGA 705
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Scoring table:

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BQ711447 BQ709526 BQ711683 BG757730

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1 ATGAGGGTCCCCGCTCCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCACGATGT
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                                                                                                                    2 DNA sequences (AAT62509 and AAT62510) respectively code for primatised forms (AAW01817 and AAW01818) of the light and heavy chain of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 7C10. Cloned 7C10 light and heavy variable genes are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of primatised antibody in e.g. CHO cells. Primatised 7B6 and 16C10 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                  monoclonal antibody binding human \rm B7.1~or~B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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4.3e-167;
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100.0%; Pred. No. 4.3
ive 0; Mismatches
                                                                                          Claim 7; Fig 8A; 81pp; English
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This sequence encodes a primatized form of the antibody 7C10 light chain from an acaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune host diseases, B cell lymphoma, infections (including by human immune also be used as imaging agents and as vaccines or immunogens to develop anti-diotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits antiden-specific immunosuppress.
                                                                                                                                                                                                        CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Teell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
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661 GGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCATGA 705
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100.0%; Pred. No. 4.3e-167;
ive 0; Mismatches 0;
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                                                                                                                                                                      Macaque primatized 7C10 light chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cells, e.g. graft rejection or tumours
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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SIDSI/gggdata/geneseq-geneseqn-embl.Na2001a.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA2002.DAT/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2003.DAT N_Geneseq_19Jun03:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 2

Description	Primatised anti-hu Macaque primatized DNA sequence of a Ant-CD4 monkey-hum Human bladder tumo DNA encoding monoc DNA encoding movel Macaque primatized
ΠD	AAT65509 AAV33484 AAS1242 AAT62867 AAZ24627 ABX12862 AAS83482
DB	1222224 222224 232222
% Query Match Length DB	705 705 705 705 926 699 833 711
% Query Match	100.0 100.0 100.0 83.0 82.6 79.2 78.8
Score	705 705 705 585.2 582.6 558.6 555.6

	CDNA CDNA CDNA CDNA CDNA CDNA CDNA CDNA	EC 44 8 E4460
40464	ABSG340 AAS224727 AAS22481872727 AAS224818 AAS22548 AAS13356 AAS1336 AAS1336 AAS1336 AAS1336 AAS1336	ABC03503 AAH818 AAC0308 AAC0508 AAC6652 AAC6652 AAC6652 AAC695 AAC695 AAC695 AAC695 AAC695 AAC695 AAC695 AAC6937 AAC6937 AAC695 AAC6937 AAC6937 AAC6937 AAC6937 AAC6937 AAC6937
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Primatised anti-human B7.1 antigen antibody 7C10 light chain DNA.
                                                                                                                     Monoclonal antibody; cynomolgus monkey; macaque; 7c10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lugus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
                        AAT62509 standard; DNA; 705 BP.
                                                                                                                                                                                                                                                                                                96WO-US10053
                                                                                                                                                                                                                                                                                                                       95US-0487550
                                                                                                                                                                                                           Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                         (first entry)
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                                                                        25-MAY-1997
                                                                                                                                                                                                                                                                       19-DEC-1996.
                                                AAT62509;
RESULT 1
             AAT62509
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Shestowsky WS;

Brams P, Hanna N,

Anderson DR,

FEATURES Location/Qualifiers source 1.705 Action 162 a 214 c 207 g 122 t ORIGIN	Query Match Best Local Similarity 100.0%; Score 705; DB 6; Length 705; Best Local Similarity 100.0%; Pred. No. 1.2e-162; Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 ATGAGGGTCCCGGTGAGCTCCTGGGGTCCTGGGTCCTGGGTGCAGGATGT 60 Db 1 ATGAGGGTCCCTGGGGGTCCTGGTGGTCTGGGTCCCAGGTGAACAATGT 60	GCCTATGAACTGAGCCACCTGGTGTGCAGTGTCCCCAGGACAGAGGGCCAGGATC	Db 121 ACTGTGGGGAGACAACAGTACAAATGAATATGTCCACTGGTACCAGCAGAACCCAGG 180 Qy 181 CGGGCCCTATACTGGTCATCATGATGATGACACGGCCCTCAGGGATCCTGAGGGA 240 Db 181 CGGGCCCTATACTGGTCATCATGATGATGATGACGGCCCTCAGGGATCCTGAGGGA 240	OY 241 TICTCIGCTCCAAATCAGGAACACCGCCACCTGACCATCAACGGGGTCGAGGCCGGG 300	361	9y 421 CCGCCTCTCTGAGGAGCTTCAAGCCAACAGGCCACACTGGTGTGTCTCATAAGTGAC 480 111111111111111111111111111111111111	QY 481 TICIACCGGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGA 540 L	QY 541 GTGGAGACCACCACCACCAAACAAAGCAACAAGAGTACGGGGCCAGCAGCTACCTG 600 [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	OY 601 AGCTGAGGCGTGAGGAAGTGCCACAGAAGCTACAGGTGCAGGTCACGCATGAA 660	Oy 661 GGGAGCACCGTGGAGACAGTGGCCCCTACAGAATGTTCATGA 705	RESULT 3 BD06334 LOCUS DEFINITION Identification of unique binding interactions between certain artibodies and the human B7.1 and B7.2 co-stimulatory antigens. ACCESSION BD063034.1 GI:22608637 VERSION BD063034.1 GI:22608637 KEYWORDS JP 2001504699-A/1. SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM EDKAryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo. REFERENCE I (bases 1 to 705) AUTHORS Anderson, D. R., Hanna, N., Brams, P. and Hard, C.
FEATURES Location/Qualifiers source 1.705 BASE COUNT 162 a 214 c 207 g 122 t ORIGIN	Ouery Match Best Local Similarity 100.0%; Score 705; DB 6; Length 705; Best Local Similarity 100.0%; Pred. No. 1.2e-162; Matches 705; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY ATGAGGGTCCCGGTCAGGTCTGTGGTCTGTGTTCTGGTTCCAGGTGCAGTGT 60	QY 61 GCCTATGAACTGAGCCACCCTCGGTGTCAGTGTCCCCAGGACGGCGGGCG	121 181 181	Py 241 TTCTCTGGCTCCAAATCAGGGAACACCGCCACCCTGACCATCAACGGGGTCGAGGCCGGG 300		OY 421 CCGCCTCCTCTGAGGAGCTTCAAGCCAACAAGGCCACACTGGTGTGTCTCATAAGTGAC 480	QY 481 TTCTACCCGGAGCCGTGACAGTGGCCTGGAAGGCAGATAGCAGCCCGTCAAGGCGGGA 540	QY 541 GTGGAGACCACCACCAAACAAAGCAACAACAAGTACGCGGCCAGCAGCAGCTG 600	QY 601 AGCCTGACGCCTGAGCAAGTCCCACAGAAGCTACAGCTGCCAGGTCACGCATGAA 660	Qy 661 GGGAGCACCGTGGAGAGACAGTGCCCCTACAGAATGTTCATGA 705 	AR265196 LOCUS AR265196 AR2651

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model Run on: October 2, 2003, 13:01:50 ; Search time 1851.84 Seconds (without alignments) 15574.362 Million cell updates/sec 15574.362 Million cell updates/sec 105-9-758-173-1 Sequence: 1 ATGAGGGTCCCGGTCAGGTTCCCCTACAGAATGTTCATGA 705 Scoring table: IDENITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 2888711 seqs, 20454813386 residues Total number of hits satisfying chosen parameters: 5777422 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
OM nucleic - n Run on: Title: Perfect score: Sequence: Scoring table: Scarched: Total number of Minimum DB seq Maximum DB seq	Post-processi

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/2/pubpna/PCUS_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-124-905-1
US-10-073-138-1
US-10-211-357-5
US-10-225-108A-11
US-09-972-656-95
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ALIGNMENTS

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NESCUTT 1
Sequence 1, Application US/09948429B
Sequence 1, Application US/09948429B
Sequence 1, Application US/09948429B
Sequence 1, Application DETTEL 18
TITLE OF INVENTION: DETTEL 18
TITLE OF INVENTION: DETTEL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: DETTEL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: DETAILS COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: DANK, SWECKER 6 MATHIS
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, PRARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESANTS"
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                                                                                                                            E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
             Darrell R.
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IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TRNGTH: 705 base pairs
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             Anderson,
                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                100.0%; Score 705; DB 10; Length 705; 100.0%; Pred. No. 3.5e-198; Live 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 GGGAGCACCGTGGAGAGACAGTGGCCCCTACAGAATGTTCATGA 705
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INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS; not relevant
                                                                                                                                                                                                                                                                                                 705; Conservative
                                                                                                                                                                                            mat_peptide
                                                                                                      MOLECULE TYPE: peptide
                                                                                            linear
                                                                                                                                                            1..705
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                           NAME/KEY:
                                                                                                                                                            LOCATION:
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US-09-948-429B-1
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Gaps ö Protein sequence

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polypeptide anti-TIMP-1 anti-TIMP-1

Human Human Human

Perfect score: Sequence:

OM protein -

Run on:

Scoring table:

Searched:

Minimum DB : Maximum DB :

Database :

Human arti-TimiAnti-Cbd0 monoclon
Anti-Cbd0 monoclon
Euman secreted pro
Euman novel protei
Euman cancer assoc
Novel human diagno
Human antibody fra
Human Ev molecule
VbJC regions of hu
Antibody protein #
Human secreted pro
Human EST encoded
Novel human diagno
Human bone marrow
Human anti-TYME-1

Monoclonal rabies Human IgG anti-rhe

Novel human diagno Anti-HIV-1 recombi Human anti-TIMP-1 Human anti-TIMP-1

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Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primatised anti-human B7.1 antigen antibody 7C10 light chain.
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  AAU11645
ABP41361
AAW01821
ABR01497
ABR01474
ABR01478
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ABP63052
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AAU08381
AAU82012
AAU4472
AAB43979
ABG19294
ABG19294
ABG78152
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AAM23527
ABG19297
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ABR01473
ABU08021
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AAR42163
ABG23083
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  96WO-US10053
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Chimeric Homo sapiens.
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(IDEC-) IDEC
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 Novel human diagno
Novel human diagno
Human novel protei
Macaque primatized
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Ant-CD4 monkey-hum
Monoclonal rabies
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                                                                                        ; Search time 27.4586 Seconds (without alignments) 1352.654 Million cell updates/sec
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1243
1 MRVPAQLLGLLLMLPGARC.......CQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT;
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           1107863 seqs, 158726573 residues
                                                                                       2003, 08:56:23 ;
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                                                            protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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ABG19295
ABG19299
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AAW63764
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                 2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human b7.1 antigen monoclonal antibody 7CLD. Cloned 7ClD light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibody in e.g. CHO cells. Primatised 7B6 and 16510 anti-B7.1 antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell./B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                                                                                                                                                                    1 MRVPAQLLGLLLLMLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA
                                                                                                                                                                                                                                                                                                                                                   RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG
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                                   Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -useful for treating autoimmune disease or graft-versus-host disease
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1e-70;
nes 0; Indels 0;
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100.0%; Pred. No. le-
ive 0, Mismatches
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                                                                   Claim 6; Fig 8A; 81pp; English.
                                                                                                                                                                                                            and graft-versus-host disease,
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WPI; 1997-108638/10.
N-PSDB; AAT62509.
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This sequence represents a primatized form of the antibody 7C10 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipons and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autofinmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and and interleukin-2 (IL-2), T cell proliferation and and interactions and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RAPILVIYDDSDRPSGIPBRFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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100.0%; Pred. No. 1e-70;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                     cells, e.g. graft rejection or tumours
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                                                                                                                                                                                                                                                Example 7; Fig 3a; 87pp; English.
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Chimeric - Macaca sp.
Synthetic.
WPI; 1998-286601/25.
N-PSDB; AAV35484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 AA;
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Is lambda chain - human C; Species: Homo sapiens (man) C; Date: 22.Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000 C; Accession: 525756

By: Combriato, G: Klobeck, H.G.

Bur: J. Immunol.-21, 131-1522, 1991
A; Reference number: 816439; MUID: 91257162; PMID: 1904362
A; Reference number: 816439; MUID: 91257162; PMID: 1904362
A; Residue; preliminary; translation not shown A; Residues: 1-23 cCOM>
A; Cross-references: EMBL: X57821; NID: 933741; PIDN: CAA40958.1; PID: 933742
C; Superfamily: Immunoglobulin V region; Immunoglobulin homology
C; Keywords: heterotetramer; Immunoglobulin homology cIMM>
F; 147-215/Domain: Immunoglobulin homology cIMM>
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CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiSpecies: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
CiSpecies: 255-47
R;Combriato, G.; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin
A;Reference numbda: S16439; MUID:91257162; PMID:1904362
A;Accession: S25747
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Listing first 45 summaries
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Accession: S25753
R; Combriato, G; Klobeck, H.G.
Bur. J. Immunol. 21, 1513-1522, 1991
A; Title: Vlambda) and J(lambda)-C(lambda) gene segments of the human immuno A; Title: Vlambda) and J(lambda)-C(lambda) gene segments of the human immuno A; Title: Vlambda; MuD: 91257162; PMID: 1904362
A; Status: Preliminary; translation not shown
A; Residues: I-231 <COM>
                                                                                                                                                                                                                                                                                                                                                                                        1 MAWIPLFLGVLAYCTGSVASYELTQPPSVSVSPGKTASITCSGDKLGDKYASWYQQKAGQ
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R;Combriato, G:; Klobeck, H.G.

Bur. J. Immunol. 21, 1313-1522, 1991

A;Title: V(lambda) and J(lambda) C(lambda) gene segments of the human immu A;Reference number: $16439; MUID:91257162; PMID:1904362

A;Accession: $25751

A;Accession: $25751

A;Residues: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-231 <COMD.

A;Residues: 1-231 <COMD.

A;Cross-references: EMBL:X57816; NID:933731; PIDN:CAA40953.1; PID:933732

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin homology <CMM>
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Pred. No. 5.3e-57;
7; Mismatches 21
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78.5%; Pre
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Matches 183; Conservative
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C; Species: Homo sapiens (man)

C; Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C; Accession: 825738

R; Combriato, G; Klobeck, H.G.

Bur. J. Immunol. 21, 1513-1522, 1991

A; Title: V(lambda) and J(lambda) C(lambda) gene segments of the human immunoglobulin lam

A; Reference number: S16439; MUID:91257162; PMID:1904362

A; Accession: 825738

A; Status: preliminary; translation not shown

A; Molecule type: mRNA

A; Residues: 1-231 < COM-

A; Residues: 1-231 < COM-

A; Cross-references: EMBL:X57802; NID:933701; PIDN:CAA40940.1; PID:933702

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer: immunoglobulin homology < CIMM>
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C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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1g lambda chain - human
1g.Species: Homo sapiens (man)
C;Species: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
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                                         PID: 933724
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                           A)Cross-references: EMBL:X57812; NID:933723; PIDN:CAA40949.1; P:C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F:148-216/Domain: immunoglobulin homology <IMM>
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.5e-60;
es 20; ]
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Pred. No. 2.5e-58;
3; Mismatches 21;
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Pred. No. 1.5e
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13; Mismatches
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80.3%;
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Best Local Similarity 85.18
Matches 194; Conservative
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Best Local Similarity 80.38
Matches 187; Conservative
              -233 <COM>
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PID: q33736

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SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINE-71150336; PubMed-5549568;
Ponstingl H., Hess M., Hischmann N.;
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MEDLINE-95255298; PubMed-7737190;
Stoppini M., Bellotti V., Negri A., Merligi G., Garver F., Ferri G.;
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MEDLINE-74109253; PubMed=4814727;
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MEDLINE=70166723; PubMed=4909564;
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10. CLEATED
10. CLEATED
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 02, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
16-SEP-2003 (Rel. 42, Last annotation update)
17-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
19-SEP-2003 (Rel. 42, Last annotation update)
19-
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MEDLINE-69088380; PubMed-4883841;
Milstein C., Clegg J.B., Jarvis J.M.,
"Immunoglobulin lambda-chains. The complete amino acid sequence abence-Jones protein.";
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  P01709
P06319
P04208
P01706
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P01712
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Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
                                                                                                                                                                                                                                                                                     ALIGNMENTS
1.V2F_HUMAN

1.V5E_HUMAN

1.V2C_HUMAN

1.V2C_HUMAN

1.V2L_HUMAN

1.V2L_HUMAN

1.V2L_HUMAN

1.V2L_HUMAN

1.V2B_HUMAN

1.V2B_HUMAN

1.V2B_HUMAN

1.V2D_HUMAN

1.V2D_HUMAN
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LV5A_HUMAN
LV4C_HUMAN
LAC_PIG
LAC1_MOUSE
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Gapop 10.0 , Gapext 0.5
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Hieter P.A., Hollis G.F., Korsmeyer S.J., Waldmann T.A., Leder P.,;
"Clustered arrangement of immunoglobulin lambda constant region genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY OF MCG.
MEDLINE-90133913; PubMed-2515285;
Ely K.R., Herron J.N., Harker M., Edmundson A.B.;
"Three-dimensional structure of a light chain dimer crystallized in where. Conformational flexibility of a molecule in two crystal forms.";
                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF NEWM.
MEDLINE-75046825; PubMed=4215080;
Poljak R.J., Amzel L.M., Avey H.P., Chen B.L., Phizackerley R.P.,
Saul F.;
"The three-dimensional structure of the fab' fragment of a human
myeloma immunoglobulin at 2.0-A resolution.";
Proc. Natl. Acad. Sci. U.S.A. 71:3440-3444(1974).
Characterization of the two unique human anti-flavin monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Rotational allomerism and divergent evolution of domains in immunoglobulin light chains."; Biochemistry 14:3953-3961(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MCG.
Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,
Panagiotopoulos N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:antigen binding activity; NAS. P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE (BENCE-JONES PROTEIN MCG).
MEDLINE-75013804; Pubbed=4415202;
Fett J.W., Deutsch H.F.;
Prinary structure of the Mcg lambda chain.";
Biochemistry 13:4102-4114(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00253; AAA59107.1; -
EMBL; L38652; AAB5681.1; ALT_INIT.
EMBL; X51754; CAB38569.1; ALT_INIT.
EMBL; X51755; CAA36049.1; -
PIR; X51755; CAA36049.1; -
PIR; A92057; L2HU
PIR; A92057; L2HU
                        immunoglobulins.";
Eur. J. Biochem. 228:886-893(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Biol. 210:601-615(1989).
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Genew; HGNC:5856; IGLC2.
Genew; HGNC:5857; IGLC3.
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PDB; 1AQK; 04-FEB-98.
PDB; 1LIL; 15-MAY-97.
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GO:0006955;
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130 QPKAAPSVTLEPPSSEELQANKATLVCLISDEYPGAVTVAWKADSSPVKAGVETTTPSKQ 189
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                                                             Immunoglobulin C region; Bence-Jones protein;
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MEDLINE-69315835; PubMed=2501791;
MILIS G.F., Evans R.J., Stafford-Hollis J.M., Korsmeyer S.J.,
MCKearn J.P.;
"Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 are
expressed in pre-B cells and may encode the human immunoglobulin
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                                                                                                    INTERCHAIN (WITH HEAVY CHAIN).
A -> N (IN MCG+ MARKER).
FTIG-VAR_003899.
S -> T (IN MCG+ MARKER).
FTIG-VAR_003899.
T -> K (IN KERN+ MARKER).
FTIG-VAR_003901.
T -> K (IN MCG+ MARKER).
FTIG-VAR_003901.
R -> K (IN MCG+ MARKER).
FTIG-VAR_003902.
R -> K (IN 02+ MARKER).
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PPC0047; Ig. 1.
SMART; SM00407; IGc1; 1.
PROSITE; PSC0835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglo
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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86.5%; Pred. No. 6.6e-83;
ive 15; Mismatches 14; Indels
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028090; AAH28090.1; -.
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           QBR062
Q99W12
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Q9RVC55
Q8RC56
Q8RC28
Q9RC6E
Q9NC6E
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Q8K1F0
Q90536
Q90524
Q8TC77
Q9TLD
Q8K1F2
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InterPro: IPR003599; IG.
InterPro: IPR007110; Ig-11ke.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003597; Ig_C1.
InterPro: IPR003596; Ig_Wr.
Pram: PP00477; Ig; 2.
SWART: SW00407; Ig; 2.
SWART: SW00407; IG; 1.
SWART: SW00406; IG, IG_WRED: SWART: SW00406; IG_WRED: SWART: SW00406; IG_WRED: IG_WRED: PROSITE; PS50835; IG_LIKE; 2.
Hypothetical protein: IG_MRC; 1.
Hypothetical protein: SEQUENCE 234 AA; 24792 MW;
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                                                                     2, 2003, 08:56:23 ; Search time 22.6452 Seconds
                                                                                                             US-09-758-173-2
1243
1 MRVPAQLLGLLLLWLPGARC......CQVTHEGSTVEKTVAPTECS 234
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Q8tbc9 homo s
Q8n5f4 homo s
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Q8nek1 homo
Q9d8w4 mus n
Q8nek0 homo
Q8tcd0 homo
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                                                                                                                                                                                                                    830525
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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                                                                                                                                                                                           830525 segs, 258052604 residues
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                                             OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Q8WUK3
Q99M11
Q8TCJ5
Q8VCP0
Q8VCP0
Q8NEK1
Q9DBW4
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Q8NSF4
Q96169
Q8WUK4
Q8NEJ1
Q8WTU6
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_organelle:*
sp_phage:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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                                                                                                                                                                                                                                                                                                                SPTREMBL_23:*
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Match 1
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474.5
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Gaps

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67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 LLGLLLLWLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPARAPILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymorean (Frocein. 19)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidee, Homo.
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N (11)
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N (11)
C TISSUE-B-cell;
A Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
R (11)
R (11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.3%; Score 961; DB 4; Length 233; 80.3%; Pred. No. 3e-76; Live 16; Mismatches 29; Indels
                                                                        Indels
                                                                                                              EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 178; Conservative
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[1]
SEQUENCE FROM N.A.
TISSUE-Brain, and Lung;
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Best Local Similarity
Matches 183; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 LLWLP------GARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHP-VFGGGTRV
                                                                                                                                TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTT
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Hymocospiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                                                                   186 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                      186 PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC022333: AAH22023.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR03356; Ig_V.
Ffam: PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE: PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBTBC9; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-JUN-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein. Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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Best Loca Matches

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Q8N5F4

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Sequence 16, Appl Sequence 17, Appl Sequence 8, Appl Sequence 26, Appl Sequence 24, Appl Sequence 20, Appl Sequence 153, Appl

4, Appli 2, Appli 6, Appli 6, Appli 6, Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Sequence 2, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: "MONKEY MONCCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teekin, Robin L.
REGISTRATION NUMBER: 012712-131
TELEPRICE/DOCKET NUMBER: 012712-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 1243; DB 3;
100.0%; Pred. No. 1.2e-102;
ive 0; Mismatches 0;
E: BURNS, DOANE, SWECKER & MATHIS 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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     ; MOLECULE TYPE: protein US-08-487-550-2
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STREET: 69
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  Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 10, Appl
Sequence 10, Appl
Sequence 4, Appli
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Sequence 1
Sequence 2
Sequence 3
Sequence 8
Sequence 2
Sequence 2
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1 MRVPAQLLGLLLMLPGARC.....CQVTHBGSTVEKTVAPTECS
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/cgn2_6/ptcdata/1/jaa/5B_COMB.pep:*
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/cgn2_6/ptcdata/1/jaa/PcTUS_COMB.pep:*
                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-526-098-2

US-08-487-589-10

US-09-526-098-10

US-09-049-672A-1

US-09-049-672A-1

US-08-049-672A-1

US-08-049-672A-1

US-08-049-672A-1

US-09-049-672A-1

US-09-049-672A-1

US-09-049-672A-1

US-09-049-672A-1

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US-09-152-060-88

US-08-977-146-22
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB :
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Length 234; Indels ,09

1 MRVPAQLLGLLLUMLPGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA 60

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Sequence 56, Appl

US-08-422-093-9 US-08-422-112-9 US-09-313-942-14 US-09-025-769B-170 US-07-916-098A-56

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67 IYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFGGGTRVT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 VLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTTP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
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                                                                         181 VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Newman, Roland B.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOARE,
ADDRESSE: BURNS, DOARE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.7%; Score 1015.5; DB 3;
86.0%; Pred. No. 1.7e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08523894
Patent No. 6136310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TRIEDHONE: 703-836-6630
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22314:3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 86.0 Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 233 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-523-894-6
                                                                                                                                                                                                                                                                                                                                                               Alexandria
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US-08-487-550-10
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                 GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                           VETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS
                                                                                                                                              Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 4;
1.2e-102;
                                                                                                                                                                                                                                                                                                                                                            STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1243;
100.0%; Pred. No. 1.2
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                         Sequence 2, Application US/09526098
Patent No. 6492134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
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APPLICATION NUMBER:
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APPLICANT: Anderso
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CLASSIFICATION:
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Best Local Simi
Matches 234;
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2, 2003, 09:18:44; Search time 87.8457 Seconds (without alignments) 421.442 Million cell updates/sec
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Sequence 2, App
Sequence 6, App
Sequence 96, App
Sequence 10, App
Sequence 10, App
Sequence 10, App
Sequence 11, App
Sequence 51, App
Sequence 31, App
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                                                                                                     US-09-758-173-2
1243
1 MRVPAQLLGLLILWLPGARC.......CQVTHEGSTVEKTVAPTECS 234
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                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to be score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-124-807-2
US-10-211-357-6
US-10-211-357-6
US-09-948-429B-10
US-09-948-429B-10
US-10-214-807-10
US-10-21-532-10
US-10-21-532-10
US-10-21-532-10
US-09-979-1534-51
US-09-972-656-98
US-10-310-119-36
                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                  587654 seqs, 158212981 residues
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                                                                                                                                                                                                                                                                                                        Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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81.7
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Sequence 2, Application US/09948429B

Patent No. US2002017689A1

GENERAL INFORMATION: MONEY WOOLCONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street

CITY: Alexandria
                                                                                                                                                                                                                                                                            sequence 70, Appl
Sequence 70, Appl
Sequence 88, Appl
Sequence 88, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 901, Appl
                                                                                          Sequence 6, Appliseduence 202, Appliseduence 88, Appliseduence 88, Appliseduence 38, Appliseduence 38,
                                                                                                                                                                                  Sequence 90, Appl
Sequence 57, Appl
Sequence 108, Appl
Sequence 82, Appl
                                                     Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
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COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
1 US-10-225-108A-14

1 US-09-972-656-102

US-09-747-669-6

US-10-194-801-6

US-09-747-669-6

US-09-972-656-90

US-09-972-656-90

US-09-972-656-90

US-09-972-656-90

US-09-972-656-90

US-09-972-656-90

US-09-9853-161-80

US-09-8852-797-70

US-09-8852-797-70

US-09-8852-797-88

US-09-8853-161-80

US-09-10-299A-7

US-09-291-299A-7

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-291-299A-10

US-09-791-299A-10

US-09-791-299A-10

US-09-791-299A-10

US-09-791-299A-10

US-09-791-6-882-742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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SQUENCE 2. Application US/10291532

SQUENCE 2. Application US/10291532

Publication No. US20030180290A1

GENERAL INFORMATION:

APPLICANT: HARLHARAN, KANDASAMY

APPLICANT: HARLHARAN, NABIL

TITLE OF INVENTION: ANTI-CD80 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC

TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OF INVENTION: COMBINATION WITH OTHER THERAPIES

FILE REPERROR: 037003/291872

CURRENT APPLICATION NUMBER: US/10/291,532

CURRENT FILING DATE: 2001-11-12

PRIOR FILING DATE: 2001-11-09

PRIOR FILING DATE: 2001-01-12

PRIOR FILING DATE: 1999-08-26

PRIOR APPLICATION NUMBER: 08/383,916

PRIOR FILING DATE: 1995-06-07

PRIOR APPLICATION NUMBER: 08/383,916

PRIOR FILING DATE: 1995-08-26

PRIOR FILING DATE: 1995-08-26

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ. ID NOS: 12
                                                                                                                                                                                                                                                                                                   61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTRVTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: primatized peptide sequence (Synthetic 102-101-231-532-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·.
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                                                                                                           Length 234;
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100.0%; Pred. No. 4.8e-92;
tive 0; Mismatches 0; Indels
                                                                                                                                                  Indels
                                                                             ,; DB 12;
4.8e-92;
0;
                                                                                                    100.0%; Score 1243;
100.0%; Pred. No. 4.8
live 0; Mismatches
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                                                                                                       Ouery Match 100.
Best Local Similarity 100.
Matches 234; Conservative
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234; Conservative
                                           protein
                      TOPOLOGY: linear
                                             MOLECULE TYPE:
                                                                US-10-124-807-2
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Best Local S
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
AURERSPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Abxandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                          61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RAPILVIYDDSDRPSGIPERFSGSKSGNTATLTINGVEAGDEADYYCQVWDRASDHPVFG 120
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                                                                                                                                                                                                                                                                                                                       1 MRVPAQLIGILILMI.PGARCAYELTQPPSVSVSPGQTARITCGGDNSRNEYVHWYQQKPA
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 VETTTPSKOSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 234;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OFFWARE: Patentin Release #1.0, Version #1.30 APPLICATION DATA:
APPLICATION WUMBER: US/10/124,807
                                                                                                                                                                                                              100.0%; Score 1243; DB 10. 100.0%; Pred. No. 4.8e-92; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULT 2
US-10-124-807-2
Sequence 2, Application US/10124807
; Publication No. US20030166207A1
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELEFAX: 703-830-20-2
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
TYPE: linear
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Matches 234; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                     US-09-948-429B-2
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October 2, 2003, 13:01:50; Search time 3758.85 Seconds (without alignments) 15574.362 Million cell updates/sec
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1431
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	AR108863 Sequence BR063035 Identific AR108867 Sequence BR063039 Identific AR40389 Sequence AR098516 Homo sapi AR135375 Sequence AR097755 Homo sapi AR135375 Sequence AR097755 Homo sapi BR060501 Process f AR135375 Sequence AR097859 Homo sapi BR060501 Process f AR097859 Homo sapi AR11959 Sequence AR097859 Homo sapi AR119685 Sequence AR06189 Sequence AR06189 Sequence AR06189 Sequence AR06189 Sequence AR076260 Sequence AR06199 Sequence AR06199 Sequence AR06196 Sequence AR076262 Homo sapi BR075127 Method fo AR097010 Homo sapi AR172957 Homo sapi	linear PAT 14-FEB-2001 stowsky,W.S. and Heard,C.
SUMMAKIES B ID	AR108863 AR265197 AR265197 BD063035 AR108867 AR35359 AR49389 AR49389 AR49389 AR735375 AR335375 AR33537	ent US 6113898. 5139 5.139 7. Hanna, N., Sheepring antibod. 1 ibodies A 3 05-SEP-2000;
% Query re Match Length D	33.1 1.1. 1.000 1.1. 1.000 1.2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2.	AR108863 Sequence 3 from patent AR108863 AR108863.1 GI:128251: Unknown. Unknown. Undassified. 1 (bases 1 to 1431) Anderson,D.R., Brams Fuman B7.1-specific prespressing said antibopatent: US 6113898-A.
Result. No. Sco	4402.24244428.242444428.2424444444444444	RESULT 1 AR108863 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL

FEATURES SOURC BASE COUNT	Location/Qualifiers		QY 961 CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAG 1020 Db 961 CGGGAGGAGCAGTACAACAGCACGTGTGGTCACCGTCCTCACCGTCCTCACCGTCTCACCACCAGCGTCCTCACCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCACCAGCAG
Query Best Match	/ Match Local Similarity 100.0%; Score 1431; DB 6; Length 1431; hes 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	· ·	1021 GACTGGCTGAATGGCAAGGAGTACAAGTCCCAAGAACTCCAACAAAGCCCTCCCACCCCC 1
Oy Dp	AGCTCCCAGATGGGTCCTGT 	•	ATCGAGAAACCATCTCCAAAGCCAAGGCAGCCCGAGAACCACAGGTGTACACCTG 1
oy Op	61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCGGCACC 120 		1141 CCCCCATCCCGGGATGAGCTGACCAGGACCAGGTCAGCTGACCTGGCTGG
Qy Dp	1 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTACTGGACCTGGATCCGCAGACC 18		1201 TTCTATCCCAGGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTAC 1
oy Op	181 CCAGGGGGGCTGGGGTTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC 240 		1261
da Db	241 AATCCTCCCTCAAGAGTCGAGTCACCATTTCAAAAGACACGTCCAAGAACCAGTTCTTC 300 		1321 GTGGACAGAGCAGGTGGCAGGAACGGAACGTCTCTCAGGTGGACGCTGAACGGATGAGGAGAAGAGAAGAAGAAGAAGAAGAAGAAGAAGA
oy G	301 CTGAACTTGAATTCTGTGACGGACACGGCCGTCTATTACTGTGCGAGAGGCCCT 360 		OY 1381 CTGCACACACACAGACAGACTCTCCCTGCTCTCCGGTAAATGA 1431 Db 1381 CTGCACACACAGAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1431
oy do	361 CGCCCTGAITGCACAATTGTTATGGCGGCTGGGTCGATGTCTGGGGCCCGGGAGAC 420		AR265197
Qy	421 CTGGTCACCGTCTCCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTC 480		110N Sequence 3 Ifom parent us 049213. ION AR265197.1 GI:29693618 DS
Oy Dp	481 TCCAAGAGCACCTCTGGGGCACAGGGCCCTGGCCTGCCTG		_
oy do	541 GAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACCTTCCCG 600		Aquin, S. and Method for I Patent: US (
Qy Db	601 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 660		SOUTCE 1.14.31 /organism="unknown" BASE COUNT 322 a 469 c 380 g 260 t
Qy Db	661 AGCTIGGGCACCCAGACCTACAICTGCAACGIGAATCACAAGCCCAGCAACACCAAGGIG 720 		Query Match 100.0%; Score 1431; DB 6; Length 1431; Best Local Similarity 100.0%; Pred. No. 3.6e-278; Matches 1431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ζζ	721 GACAAGAAAGCAGAGCCCAAATCTIGIGACAAAACTCACACGAGCCCACGIGCCCAGCA 780 		OY 1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
Qy Db	781 CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCTC 840 		Oy 61 GTGAAGCTGCAGCAGTGGGGCGAAGGACTTCTGCAGCCTTCGGAGACCCTGTCCCGCACC 120
Qy Db	841 ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGTGGTGAGCCACGAAGACCCT 900		0y 121 TGCGTTGTCTCTGGTGGCTCCATCAGCGGTTACTACTACTGGACCTGGATCCGCCAGACC 180
Qy	901 GAGGICAAGITCAAGIGGTACGIGGACGGCGIGGAGGTGCAIAATGCCAAGACAAAGCCG 960 		OY 181 CCAGGAGGGACTGGAGTGGATTGGCCATATTATGGTATGGTGCGACCACCACTAC 240

Anti-rhesus D reco Human gamma-4 heav Human gamma-4PE he

Human gamma-4E hea Nucleotide sequenc Hepatitis C virus Human anti-RSV mon Human immunoglobul Traget plasmid Man Plasmid Glambda-1A Human anti-RSV mon Antibody D heavy c Reshaped CAMPATH-1

Human benign prost Colon adenocarcino

Minimum DB seq Maximum DB seq

Database

Total number

Searched:

Perfect score:

Sequence:

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Scoring table:

Lung cancer relate

Lung cancer relate Plasmid Hul9BHcpcd Plasmid Hul9CHcpcd

DNA sequence of a Primatised anti-hu Plasmid Glambda-1B Human colon cancer Human cDNA encodin

Human monoclonal r Macaque primatized

CDNA of the

Figures and antibod Monoclonal antibod Plasmid Hu19DHcpcd Human CDNA encodin Bicistronic chimer Human C5E10 antibo Antibody C5E10 hea Encodes heavy chai Reshaped CD4 antib

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Primatised anti-human B7.1 antigen antibody 7C10 heavy chain DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antiqen; CD28; immunosuppressive; autoimmune disease; idlopathic thrombocytopaenia purpura; systemic lupus errythematosus; rheumatoid arthritis; psorlasis; type 1 diabetes mellitus; graft versus host disease;
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AAH74680
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   Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
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   PHARM CORP.
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Macaque primatized
DNA sequence of a
Primatised anti-hu
Macaque primatized
DNA sequence of a
Human immune syste
Monoclonal antibod
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Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
                                                                                             CCCCCATCCCGGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCTTGGTCAAAGGC
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AGCITGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCCAGCAACACCAAGGTG
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                                                                     Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1431; DB 18; Length 1431; 100.0%; Pred. No. 7.2e-277; ive 0; Mismatches 0; Indels 0;
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-PSDB; AAW01818.
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1 ATGAAACACCTGTGGTTCTT......CCCTGTCTCCGGGTAAATGA 1431
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                    22781392 seqs, 12152238056 residues
                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          summaries
                                                                  nucleic search, using sw model
                                                                                                    October 2, 2003, 13:05:20
                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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length: 2000000000
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DB seq
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Perfect score:
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                                                                  OM nucleic -
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ALIGNMENTS

BX377695 1201 bp mRNA linear EST 08-WAY-2003	BX377695 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cuna clone CSODI009YJ10 3-PRIME, mRNA sequence.	BX377695	BX377695.1 GI:30439018	BØT.	Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 1201)	Li,W.B., Gruber,C., Jessee,J. and Polayes,D.	Full-length cDNA libraries and normalization	Unpublished	Contact: Genóscope	Genoscope - Centre National de Sequencage	BP 191 91006 EVRY cedex - France	Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr	Library was constructed by Life Technologies, a division of	Invitrogen. This sequence belongs to sequence cluster 7198.r For	more information about this cluster, see	http://www.genoscope.cns.fr/	<pre>cgi-bin/cluster.cgi?seq=CSODI009DE05NP1&cluster=7198.r. Contact :</pre>	Feng Liang Email : fliang@lifetech.com URL :	http://fulllength.invitrogen.com/ inVitrogen Corporation 1600
RESULT 1 BX377695/c LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT										

BX377695 BX377695 BX414495 BX414495 BQ062878 AGENCOURT BX337477 BX337477

BX377695 BX414495 BQ062878 BX337477

113

1201 1142 1020 1045

66.0 65.0 63.0 62.8

944 929.6 902 899.2

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Description

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% Query Match Length DB

Score

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Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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em_gss_vrl:*
gb_gssl:*
gb_gss2:*

SUMMARIES

1357

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/note="vector: pcMVSPORT_6; 1st strand cDNA was primed
/with a NotI-ollgo(dT) primer. Five prime end enriched,
/double-strand cDNA was digested with Not I and cloned into
Iihhrary was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX414495 Homo sapiens THYMUS Homo sapiens cDNA clone CSGCAP001YI13 3-FRYIRE, MENA sequence.

BX414495.1 GI:30637021
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                                                                                                                                                                                                                                                                         CATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGT 1417
                                                                         ATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCTCCT 1297
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 1142)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 192 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was, constructed by Life Technologies, a division of
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Matches 952; Conservative
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KEYWORDS
SOURCE
ORGANISM
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sites of the pCNVSPORT 6 vector. Library was normalized.

296 c 396 g 267 t others
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     Avenue Genoscope sequence ID : CSODIO09DE05NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1201;
                                                                                                                                                                                                                                                                                                                                                                                                                 66.0%; Score 944; DB 13; 95.8%; Pred. No. 8.8e-198; ive 17; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991; Conservative
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                Faraday
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Sequence 3, Application US/08487550;
Setent No. 6113896
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION:
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS:
TITLE OF INVENTION: MANUNOSUPPRESANTS.

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BUDNERSS:
ADDRESSEE: BUDNERSS:
COTTY: Alexandria
STATE: WA
COUNTRY: USA
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATURE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 36,030
REFERENCE/POCKET NUMBER: 37,030
REFERENCE/POCKET NUMBER: 37,030
RELEPHONE: 70-836-6620
TELEPHONE: 70-836-6620
                                                                      US-08-378-939-9

US-08-286-740-3

US-09-022-449-68

US-09-021-952A-68

US-09-121-952A-68

US-09-121-952A-68

US-08-157-101A-6

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US-08-478-967A-3

US-08-478-967A-3

US-08-478-967A-3

US-08-478-967A-3

US-08-478-967A-3

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US-08-419-866-2
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US-09-343-485A-2
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1 ATGAAACACCTGTGGTTCTT......CCCTGTCTCCGGGTAAATGA 1431
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6: /cgn2_6/ptoda=a2/2/ina/PacKfiles1.seq:*
                             GenCore version 5.1.6
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October 2, 2003, 19:53:01; Search time 283.087 Seconds (without alignments) . 12894.584 Million cell updates/sec
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1 ATGRARGACCIGTGGIICTI.......CCCIGTCTCCGGGTARAIGA 1431
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Result Query

No. Score Match Length DB ID

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2 1431 100.0 1431 12 US-10-124-807-3

3 1431 100.0 1431 12 US-10-124-807-3

5 1429-4 99.9 1431 13 US-10-124-905-3

5 1435-8 91.9 1431 12 US-10-124-905-3

8 1315-8 91.9 1431 12 US-10-124-905-1

9 1315-8 91.9 1431 12 US-10-124-905-1

9 1315-8 91.9 1431 12 US-10-124-905-1

10 1314.2 91.8 11.3 US-10-124-907-11

9 1315-8 91.9 1431 13 US-10-124-907-11

10 1314.2 91.8 14.9 14.3 US-10-124-905-11

11 1171.4 81.9 14.9 14.9 US-10-211-357-1

12 1166.6 81.5 1404 14 US-10-211-357-1

13 1166.6 81.5 1428 9 US-10-225-108A-1

15 1122.8 78.5 1428 9 US-10-225-108A-1

16 1122.8 78.5 1438 9 US-10-225-108A-1

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7	02	77.0	1599	12	US-09-873-319-445	Sequence 445, App
11	02	77.0	1599	12	US-09-960-706-704	Sequence 704, App
11	1102	77.0	1599	12	US-09-873-367C-1010	Sequence 1010, Ap
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9	1097.6	76.7	1427	13	US-10-066-895-27	27
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60	092.2	76.3	1617	10	US-09-822-830A-571	57
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ALIGNMENTS

Published_Applications_NA:*

Database :

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Sequence 3, Application US/10124807

Publication No. US20030166207A1

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, Darrell R.

TITLE DF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF RITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         CGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCCACCGTCCTGCACCAG 1020
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     781 CCTGAACTCCTGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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100.0%; Score 1431;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1431; Conservative 0; Mismatches
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
                                              TYPE: nucleic acid
STRANDEDNESS: not rele
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
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LOCATION:
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Human immunoglobul

Reshaped CAMPATH-1

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Anti-Ige antibody,
Full length heavy
Full length heavy
Human C5E10 antibody C5E10 hea
Human E27 anti-IgE
Mus musculus anti-

Amino acid sequenc E27 anti-12E antib Full length heavy Humanised 1D10 ant Humanised 1D05 ant Human anti-RSV mon Protein #2 in inve

Macaque primatized Protein sequence o

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Sequence:

Scoring table:

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Monoclonal antibody; cynomolgus monkey; macaque; 7C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idlopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primatised anti-human B7.1 antigen antibody 7C10 heavy chain
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                                                                                                   AAB81972
AAR22759
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AAW95659
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AAW95663
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ID AAW0.
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(without alignments).
1352.654 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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                                                                                                                   2 Polypeptides (AAW01817 and AAW01818) respectively comprise primatised forms of the light and heavy chains of cynomoligus monkey anti-human B7.1 antigen monoclonal antibody 7010. Cloned 7010 light and heavy variable genes (see also AAT62509 and AAT62510) are inserted into variable genes (see also AAT62509 and AAT62510) are inserted into an expression vector (pref. NEOSPLA) which contains human light and heavy chain constant region genes to allow prodn. Of the primatised antibody in e.g. CHO cells. Primatised 786 and 16610 anti-B7.1 primatised antibodies have also been produced (see also AAW01819-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPDCTIICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKHLWFFLLLVAAPRWVLSQVKLQQWGGGLLQPSETLSRTCVVSGGSISGYYWTWIRQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
monoclonal antibody binding human B7.1 or B7.2 antigen for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 100.0%; Score 2577; DB 18; Length 476; al Similarity 100.0%; Pred. No. 1.3e-146; 476; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primatized 7C10 heavy chain DNA.
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                                                                        6; Fig 8B; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                              and graft-versus-host disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Matches 476; Conserv
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This sequence represents a primatized form of the antibody 7C10 heavy chain from macaque. This sequence is used in a method which studies new macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipons and inhibits binding of these antiqens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving T cell/B cell interactions, particularly autoinmune disease, specifically continued disease, specifically continued disease, and disease, allergy and multiple sclenosis, aplastic anaemia, infections with a second continued disease, allergy and multiple sclenosis, apratic anaemia, allergy and multiple sclenosis, graft vs. Const diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents, MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and thinbits continued or interleukin-2 (IL-2), T cell proliferation and thinbits continued or interleukin-2 (IL-2), T cell proliferation and
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                                                                                                                                                                                                                                                                                                                                         New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
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Matches 476; Conservative
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                                   Macaca fascicularis
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Page 1

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- 2003 Compugen Ltd.

    protein search, using sw model

GenCore
Copyright (c) 1993
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US-09-758-173-4 2577 1 MKHIWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476 BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Scoring table: Sequence: ritle:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

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	Description	Iq qamma-1 chain C	chain	chain	chain	Ig gamma-4 chain C	Ig heavy chain pre	Ig gamma-1 chain -	Ig heavy chain V r	Ig gamma-2a chain	monoclonal antibod	Ig gamma-2a chain	_	_	Ig gamma 2a chain	Ig gamma-1 chain C	Ig gamma 2b chain	Ig gamma chain Cr	Ig gamma 1 chain c		chain	Ig gamma-2 chain C	Ig heavy chain C r	heavy	Ig gamma-1 chain C		chain		in	Ig gamma-3 chain C
SUMMARIES	ID	Вино	A23511	A60764	GZHU	G4HU	S22080	S31459 ·	869339	S37483	PC4436	S40295	G2MS11	S01321	147159	S31866	I47160	PT0207	I47158	GHRB	I47161	G2GP	C30554	G3HUWI	PS0017	PS0018	G1MS	G3MSC	G1MSM	G3MSM
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Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain	Ig gamma-2 chain C	Ig gamma-2b chain	Ig gamma 4 chain c	Ig epsilon chain C	Ig gamma-1 heavy c	Ig heavy chain pre	Ig mu chain - shee	Ig Y heavy chain (Ig mu chain precur	Ig heavy chain VHI	Ig heavy chain (DO	
G2MSA	G2MSAB	G2MSAM	S00847	PS0019	806611 .	G2MSBM	147162	538864	A49444	S04845	S25705	B46529	S14683	569340	869131	
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330	332	399	329	322	327	405	277	548	220	549	592	572	627	249	241	
43.5	43.4	43.3	43.2	43.0	42.2	41.9	41.2	35.2	35.0	30.8	29.9	28.2	27.9	27.7	27.5	
1122	1119.5	1117	1114.5	1108	1088.5	1080	1062	908	903	794.5	771	727.5	719	713.5	709.5	
30	31	32	33	34	35.	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

RESULT 1

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Ig gamma-1 chain C region - human C Species: Hower sapiens (man) consequence. The consequence of Species: Hower sapiens (man) consequence. The consequence of Species: Hower sapiens (man) consequence. The consequence of Species of S
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A; Residues: BR BBL:217370
B; Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma Biochemistry 9, 3161-3170, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq A; Reference number: A90563; MUID:71064024; PMID:5489771
A; Conference number: B90563
A; Molecule type: protein Eu A; Accession: B90563
A; Molecule type: protein
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A; Molecule type: protein
B; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
B; Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
A; Reference number: A90564; MUID:71064025; PMID:5530842
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A.Reference number: S33904
A.Accession: S3604
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A.Accession: S3604
A.Molecule type: DNA
A.References: EMBL:217370
R.Takahashi, N.; Udda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A.Title: Structure of human immunoglobulin gamma genes: implications for evolution of A.Reference number: S33887; MUID:83001943; PMID:6811139
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A; Residues: 136-154, Q', 156-165, Q', 167-176, Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2
A; Note: this sequence has the G1m(non-1) markers, 239-G1u and 241-Met
R; Ponstingl, H; Hilschmann, N.
H; Ponstingl, H; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A; Title: Die Primaerstruktur eines monoklonalen 1961-7mmunglobulins (Myelomprotein Ni
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Agosana-3 chain C region (allotype G3m(b)) - human C Species: Homo sapiens (man) C Species: Howek, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 179-1789, 1986 A STILLE: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: A, Reference number: A23511; MUID:86148507; PMID:3081877 A, Accession: A23511 A, MUID:86148507; PMID:3081877 A, Constant region gene: A, Residues: 1-377 < HUC> A, Residues: 1-377 < HUC> A, Constant C Species: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           u) with an IGHG4
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A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 81.7%; Pred. No. 5.2e-89;
Matches 308; Conservative 10; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin homology <IMM>
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       A.Reference number: A91668; MUID:77070269; PMID:826475
A.Contents: myeloma protein Nie
A.Accession: B91668
A.Accession: A.B.; Palm, W.; Hilspann, N.
Boppe-2841er's Z. Physiol. Chem. 364, 713-747, 1983
A.Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgGl KOL
A.Reference number: A91723; MUID:83289131; PMID:6884994
A.Accession: A91723
                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-96, Xr, 98-197, D', 199-238, YE', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Residues: 1-96, Yr', 98-197, D', 199-238, YE', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A; Mote: this sequence has the Glm(3) and Glm(non-1) markers
B; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A; Reference number: A90565; MUID: 71064027; MUID: 4923144
A; Contents: annotation: disulfide bonds
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
A; Reference number: A91667; MUID: 77070267; PMID: 1002129
A; Contents: annotation; disulfide bonds
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A; Introns: 99/1; 114/1; 224/1
A; Introns: 99/1; 114/1; 224/1
A; Introns: 99/1; 114/1; 224/1
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into 1a C; Superfamally: immunoglobulin credion; immunoglobulin homology
C; Reywords: duplication; 49/coprotein; heterotetramer; immunoglobulin
E; 20-85/Domain: immunoglobulin homology <IM2>
F; 243-310/Domain: immunoglobulin homology <IM2>
F; 243-310/Domain: immunoglobulin homology <IM2>
F; 27-33; 144-204, 250-308/Disulfide bonds: #status experimental
F; 103/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 109/112/Disulfide bonds: interchain (to heavy chain) #status experimental
F; 109/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
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HVC1_HETFR
HVC2_HETFR
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ALC1_GORGO
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BVC3_HETFR
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HVC3_HETFR
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US-09-758-173-4 2577 1 MKHLWFFLLLVAAPRWVLSQ......MHEALHNHYTQKSLSLSPGK 476

Title: Perfect score: Sequence:

on:

P23084 heterodontu P23085 heterodontu P23088 heterodontu P01876 homo sapien P01877 homo sapien P01824 homo sapien P01825 homo sapien P01825 homo sapien P01825 homo sapien P01825 mus musculu P18531 mus musculu P01878 mus musculu P01878 mus musculu

ALIGNMENTS

RESULT. 1	GC1_HUMAN ID GC1_HUMAN STANDARD;	P01857;	21-JUL-1986 (Rel. 01, 15-SEP-2003 (Rel. 42,	Ig gamma-1 chain renel					RN (2) RD RX MEDLINE=71064024; PubMed=				_	RN [3] RP SEQUENCE OF 136-329 (EU)		RA Rutishauser U., Cunningna	The covalent	RI acid sequence of heavy-ch	[4]		RA Ponstingl H., Hilschmann		RT MONOCLONAL 1961 INMUNOSIC	peptides and discu		RN [5] RP SEQUENCE (MYELOMA PROTEIN		Schmidt W.E., Jung	RT Three-dimensional Structure of crystallized	RL Hoppe-Seyler's Z. Physio.			
		127863					esults predicted by chance to have a to the score of the result being printed, of the total score distribution.		2000 1000 1000 1000 1000 1000 1000 1000	TOTO di TOSSO	рошоц	PUIBSY nomo sapien PO1861 homo sapien		P01862 cavia porce			P01808 mus musculu P22436 mus musculu	mus	P03987 mus musculu P01863 mus musculu		P20762 rattus norv		P01866 mus musculu	2014		P06331 homo sapien			P03988 oryctolagus			P01874 canis famil P06337 mesocricetu	. (
Gapext 0.5	47026705 residues	its satisfying chosen parameters:	C	0	Match 0% Match 100% first 45 summaries		is the number of results predicted by chance to have ter than or equal to the score of the result being prived by analysis of the total score distribution.	SUMMARIES		TD	GC1_HUMAN	GC2_HUMAN	GC_RABIT	GC2_CAVPO	GC1_RAT	. GCB_RAT	GC1_MOUSE	GCIM_MOUSE	GC3M_MOUSE	CCAB_MOUSE	L GCAM_MOUSE	GCA_RAT	GCB_MOUSE	1 GCBM_MOUSE	1 EPC RAT	1 HV21_HUMAN	I EPC_MOUSE	1 MUC_MOUSE	1 MUC_RABIT	MICH RABIT	1 MUC_SUNMU	1 MUC_CANFA	1 MUC_MESAU
BLOSUM62 Gapop 10.0 , Gap	_	its satisfying	ength: 0		Minimum Match Maximum Match Listing first	SwissProt_41:*	s the number of rer than or equal		Query	Match Length UB										43.4 335 1											. r.	ښ <i>د</i>	16.1 454
Scoring table: BI	searched: 13	Total number of h	Minimum DB seq le	ns sed re	Post-processing: Post-p	Database :	Pred. No. is score greated and is derif		Result	Score	1763	1600	1226.5	1212.5	115/	1142.5	1138	1133	1126	1119.5	1117	1108	1085	1080	483	468	2 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	441.5	5 437	431.5	n m	30 420	_

RESULT GC1_HUN ID GC	RESULT 1 GC1_HUMAN ID GC1_HUMAN	STANDARD;		PRT;	330 8	AA.	
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	15-SEP-2003 (R Ig gamma-1 cha	(Rel. 42, Last chain C region.		oration	j di	are)	
Z o	IGHG1.	(Human)					
88		azoa; Cho	Chordata; (raniat	, v	Craniata; Vertebrata; Euteleostomi;	tomi;
SS	Mammalia; Euther	eria; Pr:	imates; (Jatarrh	ini;	Hominidae; Homo.	
4 2	INCEL TAKED SOU	ò					
RP	SEQUENCE FROM N.A.	N.A.					
RX	MEDLINE=822742	38; PubMe	ed=62874	32;			
RA E	Ellison J.W., Berson B.J., Hood L.E.;	Berson B	of to en	A L.E.	anum	qamma1	gene.";
RI	Nucleic Acids	Res. 10:	4071-407	3(1982)	Ŀ		
R. N.	[2]						
я. Н	SEQUENCE OF 1-135 (MYELOMA	135 (MYE)	(MYELOMA PROTEI	PROTEIN EU)			
KX.	MEDLINE=/1064	Ditto	EG=04097	(+)	E W L	Gottlieb P.D.	
RA V	Cunningham B.A., Kucishauser U., Davdal M.T. Edelman G.M.:	A., Kucis Adelman G	M.:	יי פמדי	-	1	
Z Z	"The covalent	structur	e of a h	uman ga	ашша	G-immunoglobulin, V	VII. Amino
RT	acid sequence	of heavy	-chain c	yanoger	bro	mide fragments Hl-H	H4.";
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

sp_vertebrate:* sp_rvirus:* sp_bacteriap:* sp_archeap:*

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L Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
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R InterPro: IPR00306; Ig_MHC.
R InterPro: IPR00396; Ig_V.
R InterPro: IPR00396; Ig_V.
DR RAM: SMOR406; IGY; 1.
DR SMART; SMO0406; IGY; 1.
DR ROSITE; PS00196; COPPER_BLUE; 1.
DR ROSITE; PS00196; COPPER_BLUE; 1.
DR ROSITE; PS00290; IG_LIKE; 4.
DR ROSITE; PS00290; IG_LIKE; 4.
SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
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01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-JUNAR-2003 (TIEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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TISSUE-Kidney;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 PEPVIVSWNSGALISGVHTFPAVLQSSGLYSLSSVVIVPSSSLGTQTYICNVHKPSNTK 237
                                                                                                              357 SIEKTISKAKGOPREPOVYTLPPSOEEMTKNOVSLICLVKGFYPSDIAVEWESNGOPENN 416
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240 VDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 299
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.1%; Score 1884.5; DB 4; Length 521; 70.2%; Pred. No. 4e-151; Live 32; Mismatches 61; Indels 63;
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Straubberg R.;
Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033178; AAH33178.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003957; Ig_C1.
InterPro; IPR003066; Ig_MHC.
InterPro; IPR003596; Ig_V.
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SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-2002 (TrEMBLrel. 22, Created)
01-0cT-2002 (TrEMBLrel. 22, Last sequence update)
01-0cT-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
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SMART; SMO0407; 1Gcl; 3.
SMART; SMO0406; IGCl; 3.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
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952.662 Million cell updates/sec
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                                                                                                                                                                                                                          1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSLSPGK 476
                                                                                                               October 2, 2003, 09:12:09 ; Search time 21.1407 Seconds
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Sequence 8,
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                           328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         - protein search, using sw model
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length: 2000000000
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2577
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Match Length
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Maximum DB seq
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Sequence 4, Application US/08487550
Patent No. 6113898
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ANGERSON, Darrell R.
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILLING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 2577; DB 3;
100.0%; Pred. No. 4.6e-206;
Live 0; Mismatches 0;
US-08-466-151-8

US-09-27-449-18

US-09-026-985-71

US-09-026-985-71

US-09-234-34-08-71

US-09-234-34-08-71

US-09-68-71

US-09-68-71

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-68-148-2

US-09-301-189-3

US-09-301-59-3

US-09-301-59-3-3

US-09-301-59-3-3

US-09-301-59-3-3
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRENCE/CDOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEG ID NO: 4:
SEQUENCE CHRRACIERISFICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELEPHONE: 703-00.
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 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
 USA
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Sequence Sequence Sequence Sequence

Sequence 3

Fri Oct

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                   Matches 476; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alexandria
                                                Query Match
Best Local Similarity
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US-08-487-550-12
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       us-09-526-098-4
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TITLE OF INVENTION: "MONREY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO BURAN B7 1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE: 12
CORRESPONDENCE: ADDRESS:
                                                                                                                                                  PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
                                                                  RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVPPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                    EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                 241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
                                                                                                                                                                                                                                                                   EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 360
                                                                                                                                                                                                                                                                                                                                   IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
                                                                                                                                                                                                                                                                                                                                                                                                  421 KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: BURNS, DOANE, SWECKER & MATHIS 599 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        012712-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09526098
Patent No. 6492134
GENERL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35,030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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US-09-526-098-4
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Sequence 12, Application US/08487550

Patent No. 6113898

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: TO HUMBN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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                                                                                                                                                                                                               361 IEKTISKAKGOPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 420
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                                                                                                                                                                                                                                                                             121 RPDCTTICYGGWVDVWGPGDLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFP 180
                                                                                                                                                                                                                                                                                                                                                                         181 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 DKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP 300
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                                                                                                                     1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT
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                                                 Gaps
                                               0;
Length 476;
                                                 Indels
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CURRENT APPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995
  100.0%; Score 2577; DB 4;
100.0%; Pred. No. 4.6e-206;
ative 0; Mismatches 0;
                                            0;
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699 Prince Street
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October 2, 2003, 09:18:44; Search time 178.695 Seconds (without alignments) 421.442 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                     1 MKHLWFFLLLVAAPRWVLSQ.........MHEALHNHYTQKSLSPGK 476
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/cgn2_6/ptodata/2/pubpaa/NEO7_NEW_PUB.pep:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   587654 seqs, 158212981 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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2577
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                                                                                                                                                                                                                                                               Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

		,			SUMMARIES	
Result No.	Score	% Query Match	% Query Match Length DB I	DB	ΩI	Description
	2577	100.0	476	2	US-09-948-429B-4	Sequence 4, Appli
7	2577		476	12	US-10-124-807-4	Sequence 4, Appli
m	2577			12	US-10-291-532-4	
4	2577			14	US-10-124-905-4	
'n	2309			10	US-09-948-429B-12	Sequence 12, Appl
ø	2309			12	US-10-124-807-12	Sequence 12, Appl
7	2309			12	US-10-291-532-12	Sequence 12, Appl
œ	2309			14	US-10-124-905-12	Sequence 12, Appl
σ	2112.5			15	US-10-211-357-12	Sequence 12, Appl
10	2111.5			15	US-10-211-357-8	Sequence 8, Appli
11	2104.5			15	US-10-211-357-10	Sequence 10, Appl
12	2103			11	US-09-925-179-66	Sequence 66, Appl
13	2100			αv	US-09-920-171-14	Sequence 14, Appl
14	2100			σ	US-09-920-171-16	Sequence 16, Appl
ī,	2100			-	US-09-925-179-65	Segmence 65. Appl

Sequence 14, Appl	Sequence 16, Appl	w	1,8	w		ď		a) a)	œ	Sequence 8, Appli	~			-	_	37	41	47	5	(1)	27, AI	3	23(٠,	e)	Sequence 43, Appl		a)	21
IS-10-113-996-14	US-10-113-996-16				18-10-292-869-2	18-09-792-938-2											1	IS-10-171-452A-47	IS-10-171-452A-59	e		0	US-09-996-265-230	US-10-225-108A-3	15-09-848-832-3	-09-796-848A-43	-09-796-848A-49	16	-09-996-288-21
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81.5	81.5	81.5	81.2	81.2	81.2	81.2	80.5	80.4	0	80.4	0	80.3	0	80.3	80.0	σ	9	79.7	79.7	79.6	79.5	79.4	79.4	79.4	79.4	79.4	79.4	79.4	79.4
2100	2100	2099	2002	2092	2092	2092	2075.5	2073	2073	2073	2073	2069	2069	2069	2061.5	2055	2053.5	2053.5	2053.5	2050.5	2047.5	2047	2047	2046	2046	2045.5	2045.5	2045.5	2045.5
16	17	18	on ⊢	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-09-948-429B-4

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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCE: 12
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: USA
ZIF: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE: APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
Sequence 4, Application US/09948429B Patent No. US20020177689A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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PRIOR APPLICATION DATA:
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US-10-291-532-4
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TITLE OF INVENTION: "MONEX MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: INMINOSUPPRESANTS"

CORRESPONDENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCES: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 PLINCE SLEET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 PGRGLEWIGHIYGNGATTNYNPSLKSRVTISKDTSKNQFFLNLNSVTDADTAVYYCARGP 120
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                                                                                                                                                          Query Match 100.0%; Score 2577; DB 10; Length 476; Best Local Similarity 100.0%; Pred. No. 4.8e-179; Matches 476; Conservative 0; Mismatches 0; Indels 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/10124807; Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4.76 amino acids
TYPE: amino acids
TOPOLOGY: linear
703-836-2021
                                                                                                      MOLECULE TYPE: protein US-09-948-429B-4
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 TELEFAX:
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US-10-124-807-4
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APPLICANT: HARHARM, NABIL
TITLE OF INVENTION: ANTI-CDB0 ANTIBODY HAVING ADCC ACTIVITY FOR ADCC
TITLE OF INVENTION: MEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR IN
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
CURRENT APPLICATION NUMBER: 037003/2916/291,532
CURRENT FILING DATE: 2002-11-12
PRICA APPLICATION NUMBER: 60/331,187
PRICA FILING DATE: 2001-11-09
PRICA FILING DATE: 2001-11-09
PRICA TOWN NUMBER: 09/758,173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGXYYWTWIRQT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKHLWFFLLLVAAPRWVLSQVKLQQWGEGLLQPSETLSRTCVVSGGSISGYYYWTWIRQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 2577; DB 12; Length 476; Best Local Similarity 100.0%; Pred. No. 4.8e-179; Matches 476; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                012712-131
                                              US 08/487,550
APPLICATION NUMBER: 09/383,916
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                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                 35,030
                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                    FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                         NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-10-124-807-4
                      FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nuc	OM nucleic - nucleic search, using sw model
Run on:	October 2, 2003, 13:01:50; Search time 1891.24 Seconds (Without alignments) 15574.362 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-758-173-5 720 1 AIGAGCCICCCTGCICAGCITCAACAGGGAAGAGIGIIGA 720
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	2888711 seqs, 20454813386 residues
Total number of	Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq 1 Maximum DB seq 1	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing:	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : GenEmbl:*

1: 9D_ba:*

2: 9D_htg:*

4: 9D_ov:*

6: 9D_ph:*

8: 9D_ph:*

10: 9D_pr:*

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17: em_Dii:*

18: em_Di:*

19: em_Di:*

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21: em_Or:*

22: em_Or:*

22: em_Or:*

23: em_Di:*

24: em_Di:*

25: em_Di:*

26: em_Li:*

27: em_Ar:*

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28: em_htg_other:*

30: em_htg_other:*

31: em_htg_other:*

33: em_htg_other:*

34: em_htg_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Anderson, D.R., Hanna, N., Brams, P. and Hard, C.
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Identification of unique binding interactions between certain antibodies and the human B7.1 and B7.2 co-stimulatory antigens.
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                                                                                            100.0%; Score 720; DB 6; Lilarity 100.0%; Pred. No. 1.6e-194; Conservative 0; Mismatches 0;
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   Location/Qualifiers
                              /organism="unknown"
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   FEATURES
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Aguin,S. and Vezina.Louis.-P.
Method for producing polyhydroxyalkanoates in recombinant organisms
Patent: US 6492134-A. 310-DEC-2002;
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                                                                                                    Length 720;
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Sequence 5 from patent US 6492134.
AR265198.1 GI:29693619
                             /organism="unknown"
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JOURNAL
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AR265198
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FEATURES
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us-09-758-173-5.rng

Page 1

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GenCore version 5,1,6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

October 2, 2003, 12:12:30 ; Search time 147.469 Seconds (without alignments) 13179.730 Million cell updates/sec Run on:

US-09-758-173-5 Title:

720 1 ATGAGCCTCCCTGCTCAGCT......TCAACAGGGGAGGTGTTGA 720 Perfect score: Sequence:

IDENTITY_NUC Gapopt 1.0 Scoring table:

2552756 seqs, 1349719017 residues Searched:

Total number of hits satisfying chosen parameters:

5105512

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2000.DAT:*/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2001b.DAT:*/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2001b.DAT:*/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2002.DAT:*/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2002.DAT:*/SIDSI/gggdata/geneseq/,geneseqn.embl/NA2002.DAT:* /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*/SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:* /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:* /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Macaque primatized	DNA sequence of a	Primatised anti-hu	Anti-human Fas hum	Anti-human Fas imm	Human immunoqlobul	Anti-human Fas Iq	Anti-human Fas hum
	ID		AAS17244	AAT62511	AAV61362	AAA78270	AAV66632	AAA78320	AAV61360
	DB	19	24	18	13	21	19	21	19
	Query Match Length DB	720 19	720	720	720	720	891	891	720
ar (Query	100.0	100.0	8.66	86.4	86.4	86.2	86.2	85.9
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ALIGNMENTS

AAV35486 standard; DNA; 720 BP. (first entry) 29-SEP-1998 AAV35486; RESULT 1 AAV35486

Macaque primatized 7B6 light chain DNA.

Monoclonal antibody; Mab; macaque; light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; real, Real interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.

Macaca fascicularis.

/*tag= a /product= 7B6 light chain Location/Qualifiers 1..720 /*tag= a WO9819706-A1 14-MAY-1998. Key

97WO-US19906. 96US-0746351. 29-OCT-1997; 08-NOV-1996;

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Gaps
                                                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and Inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
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                                                                                                                                                                                                                                                                                              100.0%; Score 720; DB 19; Length 720; 100.0%; Pred. No. 2.9e-182; tive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                              Sequence 720 BP; 178 A; 200 C; 193 G; 149 T; 0 other;
                                                                                 cells, e.g. graft rejection or tumours
                                                                                                Example 7; Fig 4a; 87pp; English.
                Hanna N;
                                                                                                                                                                                                                                                                                                              720; Conservative
(IDEC-) IDEC PHARM CORP.
                Brams P,
                                WPI; 1998-286601/25.
P-PSDB; AAW63762.
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Example 8; Fig 4a; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAY-2001; 2001WO-US15364.
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                                                                                                                                                                                                                                                                                                                                                  12-MAR-2002 (first entry)
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Chimeric - Macaca sp.
Synthetic.
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                                                                                                                                                                                                             This sequence encodes a primatized form of the antibody 7B6 light chain from macaque. This sequence is used in a method which studies new monclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to MaD's are specific immunosuppressants for treatment of diseases involving 7 cell/B cell interactions, particularly autoimmune disease, specifically idiopathic thrombocycopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, Inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the NAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and and multipen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppress.
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GICACCCATCAGGGCCTGAGCTCGCCCGTCACAAGAGCTTCAACAGGGGAGAGTGTTGA 720
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481 CIGAATAACTICCTAICCCAGAGAGGCCAAAGIACAGIGGAAGGIGGAIAACGCCCICCCAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; apoptosis inducer; allerdy; CD28 receptor antagody; b7_1 antigen; CD80, b7_2 antigen; CD86, B cell cancer; metastasis; tumour; B cell lymphoma; B cell leukaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection; interleukin-2; IL-2; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; macaque monkey; light chain; primatised antibody; 7B6 antibody;
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                                                                                         541 PCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence of a primatised form of the light chain of 7B6 antibody.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I. (Dasses 1 to 816)

NIH-MGC http://mgc.noi.nih.gov/.

L. Onpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-femail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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Homo sapiens
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AUTHORS
TITLE
JOURNAL
COMMENT
    BI759427 603043095
BM007808 603617276
CB958667 AGENCOURT
BI758820 603042739
                                                                                                        2, 2003, 13:05:20 ; Search time 1190.71 Seconds (without alignments) 14696.420 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd
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Maximum Match 100%
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gb_est4:
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774
795
857
                                                                                                              October
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84.8
84.4
83.1
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Score

Result . ₽ 618.8 610.6 608 598.2

οŧ

Total number

Database

Searched:

Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

```
/note=_organ: spleen; vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRIXAhoI sites using the following 5 adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library 160 t
                                                                                                 BM007808 774 bp mRNA linear EST 30-OCT-2001 603617276F1 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:5440962 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGITGTGATGACTCAGTCTCCACTTCCCATCACACCTGGAGAGCCGGCCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACAGTAATGGAGACACCTTCCTGAGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TATCAGCAGAGACAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACGGGAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 GATGITGIGAIGACTCAGICTCCACTCTCCCTGCCGTCACCCTIGGACAGCCGGCCTCC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 TCTGGGGTCCCAGACAGATTCAGCGGCAGTGGGGCAGGGGACAGATTTCACACAGAAATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. II (bases 1 to 774)

Nat-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
      670 CTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAGGAGCTTCAACAGGGGAGAGTGTT 727
                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM1914 row: h column: 19
High quality sequence stop: 770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 TITCAGCAGAGGCCAGGCCAATCTCCCAAGGCGCCTAATTTATAAGGTITCTAACCGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGAGCCTCCCTGCTCAGCTCCTCGGGCTGCTATTGCTCTGCGTCCCCGGGTCCAGTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:5440962"
/tab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 610.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                              BM007808.1 GI:16522162
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91.6%;
                                                                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.69
Matches 657; Conservative
                                                                                                                                          mRNA sequence.
BM007808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ๙
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                                                                                                                  DEFINITION
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ORIGIN
                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                 REFERENCE
                                                             RESULT 2
BM007808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 CCCACTITCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 CGGACGTTCGGCCAAGGGACCAAGGTGGAATCAAACGAACTGTGGCTGCACCATCTGTC 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 TCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AGCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 AGCAGCACCCTGACGCTGAGCAAGCAGCTACGAGAAACACAAAGTCTACGCCTGCGAA 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AGCGCAGTGGAGGCTGAAGATGTTGGGGGTTTATTTCTGCGGGCAAGGTACAAGGACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 618.8; DB 12; Length 816;
Pred. No. 8.8e-163;
0; Mismatches 62; Indels 0;
                                                         /organism="Homo sapiens"
High quality sequence stop: 814.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.9%;
ilarity 91.4%;
Conservative
                                      .816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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Best Local 9
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Gaps

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Score 720;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: BURNS, DOANE, S
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 720 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
1..720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
1..720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Anders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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US-08-487-550-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                        2, 2003, 13:10:05; Search time 38.2657 Seconds (without alignments) 8304.972 Million cell updates/sec
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Sequence 55, 3
Sequence 55, 3
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1 ATGAGCCTCCCTGCTCAGCT......TCAACAGGGAGAGTGTTGA 720
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                                                                                                                                                                                                             1139956
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(GqD2_6/ptodata/2/ina/5A_COMB.seq:*

(GqD2_6/ptodata/2/ina/5B_COMB.seq:*

(GqD2_6/ptodata/2/ina/6A_COMB.seq:*

(GqD2_6/ptodata/2/ina/RB_COMB.seq:*

(GqD2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(GqD2_6/ptodata/2/ina/PCTUS_COMB.seq:*

(GqD2_6/ptodata/2/ina/backfiles1.seq:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-487-550-5
US-09-526-098-5
US-08-398-612A-55
US-08-398-612A-55
US-08-398-612A-55
US-08-396-851A-55
US-08-491.334A-55
US-08-804-444A-41
US-09-02-449-41
US-09-02-985-41
US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-41
US-09-121-952A-41
US-08-677-67-50
US-08-677-67-50
US-08-677-67-50
US-08-677-67-50
US-08-677-898-19
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US-08-488-376-16
US-08-634-223-16
US-08-634-224-16
US-08-634-400-16
                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          nucleic search, using sw model
                                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                   length: 0
length: 200000000
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                                                                                                                      US-09-758-173-5
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                                                                              October
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                                                                                                                                 Perfect score:
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471.
468.
468.
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468.
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Maximum DB
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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
APP1
APP1
APP
APP
APP
APP
APP
APP
APP
                                                        Sequence
Sequence
Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IPP COMPATIBLE
COMPUTER: IPP PC COMPATIBLE
COMPUTER: ISP PC COMPATIBLE
COMPUTER: ISP PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-101-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIN, RODIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 703-836-6620
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DB 3;
US-09-335-697B-16
US-09-335-697B-16
US-08-376-852-152
US-08-276-852-152
US-08-899-575-152
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-899-575-168
US-08-276-852-170
US-08-276-852-170
US-08-276-852-170
US-08-899-575-156
US-08-899-575-156
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US-08-899-575-176
US-08-899-575-176
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US-08-899-575-176
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AS

Fri Oct

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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                              720 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 720; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                                                                                                                                                                                                                                                                              CDS
1..720
                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
US-09-526-098-5
                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                 CENGTH:
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WONKEY WONCOLONAL ANVIBODIES SPECIFIC
FORTION: TO HURAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
FENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
                                                                                                    61 GAAGTTGIGATGACTCAGTCTCCACTGCCCTTCCCATCACACCTGGAGAGCCGGCCTCC 120
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                                                                                                                                                         121 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG
                                                                                                                                                                                                            181 TATCAGCAGAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACCGGGAC
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                                                                                                                                                                                                                                                                               361 CCCACTTTCGGCGGAGGGACCAAGGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA
                          0; Gaps
                        0; Indels
           Pred. No. 4e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEE: BURNS, DOANE, SWECKER & MATHIS: 699 Prince Street
Alexandria
                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMUNOSUPPRESANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCI
TITLE OF INVENTION: "MONKEY MONOCI
TITLE OF INVENTION: PHARMACTUTIAL
TITLE OF INVENTION: IMMUNOSUPPRESP
100.08; 21
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COMPUTER: IBM PC compatible
                        720; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
          Best Local Similarity
Matches 720; Conserv
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61 GAAGTTGTGATGATGATCTCCATGTCCCTTCCCATCACACCTGGAGAGCGGCCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 720; DB 4; Length 720; 100.0%; Pred. No. 4e-203; Live 0; Mismatches 0; Indels
                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                 012712-131
                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY AGENT INFORMATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                              NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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US-09-948-429B-5
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                                                          2, 2003, 19:53:01; Search time 142.434 Seconds (without alignments) 12894.584 Million cell updates/sec
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                                                                                                                      1 ATGAGCCTCCCTGCTCAGCT......TCAACAGGGGAGAGTGTTGA 720
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-291-532-5
US-10-124-905-5
US-10-124-905-5
US-10-158-646-63
US-09-992-600A-7
US-09-992-095B-7
US-09-992-095B-7
US-10-154-678-7
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US-09-972-656-91
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                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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                                                                                                                                                                          1708419 seqs, 1275431651 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                         Published_Applications_NA:*
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Query
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        11
        US-09-972-656-105
        Sequence 105, Appl 19

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        US-09-972-656-93
        Sequence 25, Appl 19

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        US-09-972-658-41
        Sequence 25, Appl 20

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        US-09-126-258-41
        Sequence 24, Appl 20

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        Sequence 41, Appl 30

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        Sequence 37, Appl 30

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        14
        US-10-171-452A-35
        Sequence 49, Appl 30

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        Sequence 57, Appl 30

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        US-10-171-452A-3
        Sequence 49, Appl 30

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        14
        US-10-1158-45A-3
        Sequence 57, Appl 30

        29
        488.8
        67.2
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Sequence 5. Application US/09948429B
Factent No. US20020177689A1
Factent No. US2002017768A1
Factent No. US2002017768A1
FACTED FUNEWATION:
FULLE OF INVENTION:
FULLE OF
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CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGAAGGTGGAAGTCCTCCAA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTCCTGTAGGTCTAGTCAAAGCCTTAAACACAGTAATGGAGACACCTTCCTGAGTTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 TATCAGCAGAAGCCAGGCCAACCTCCAAGGCTCCTGATTTATAAGGTTTCTAACGGGAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 CTGAATAACTICTATCCCAGAGGCCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAA 540
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100.0%; Pred. No. 2.2e-221;
Live 0; Mismatches 0;
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                  720; Conservative
                                                                                                                                                                                         NAME/KEY: mat_peptide LOCATION: 1..720
                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                         1..720
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                         LOCATION:
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US-09-948-429B-5
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Sequence 5, Application US/10124807; Publication No. US20030166207A1; GENERAL INFORMATION:

US-10-124-807-5

RESULT 2

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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-20N-1995
ATTORNEY, AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 09/383,916
Anderson, Darrell R.
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Matches 720; Conserv
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                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                              22314
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; LOCATION:
US-10-124-807-5
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APPLICANT:
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1352.654 Million cell updates/sec
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/SIDS1/gcgdata/geneseq/geneseqp.embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp.embl/AA1981.DAT:*
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/SIDS1/gcgdata/geneseqy-geneseqp-embl/AA1987.DAT:*
/SIDS1/gcgdata/geneseqy-geneseqp-embl/AA1987.DAT:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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10: SIDSI/gcgdata/geneseqp_embl/AA1989.DAT:*
11: SIDSI/gcgdata/geneseqy_geneseqp_embl/AA1989.DAT:*
12: SIDSI/gcgdata/geneseqy_embseapp_embl/AA1990.DAT:*
13: SIDSI/gcgdata/geneseqy_embl/AA1991.DAT:*
14: SIDSI/gcgdata/geneseqy_embl/AA1991.DAT:*
15: SIDSI/gcgdata/geneseqy_embl/AA1992.DAT:*
16: SIDSI/gcgdata/geneseqy_embl/AA1995.DAT:*
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20: SIDSI/gcgdata/geneseqy_embseapp_embl/AA1999.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	Primatised anti-hu		Protein sequence o						
SUMMARIES	ID	AAW01819	AAW63762	AAU11540	AAW71879	AAB12916	AAW71877	AAW71878	AAB12914	AAB12915
	DB	18	19	23	19	21	19	19	21	21
	Query Match Length DB 1	239	239	239	239	239	239	239	239	239
di	Query	100.0	100.0	100.0	6.68	6.68	9.68	9.68	89.6	89.6
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Monoclonal antibody; cynomolgus monkey; macaque; 7B6; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenia purpura; systemic lupus erythematosus; rheumatoid arthritis; psoriasis; type 1 diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma.
                                                                                               Primatised anti-human B7.1 antigen antibody 7B6 light chain.
                                                                                                                                                                                                                                                                                                                                                                            Shestowsky WS;
                     AAW01819 standard; Protein; 239 AA
                                                                                                                                                                                                                                                                                                                                                                            Anderson DR, Brams P, Hanna N,
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                                                                                                                                                                                                             Chimeric Macaca cynomolgus;
Chimeric Homo sapiens.
                                                                         (first entry)
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                                                                        25-MAY-1997
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody, Mab, macaque, light chain; primate; antigen; CD80; CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; Tell/R sell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idlotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation.
                                                                                                                                                 2 Polypeptides (AAW01819 and AAW01820) respectively comprise primatised forms of the light and heavy chains of cynomolgus monkey anti-human B7.1 antigen monoclonal antibody 786. Cloned 786 light and heavy variable genes (see also AAT62811 and AAT13847) are inserted into an expression vector (pref. NBOSPLA) which contains human light and heavy chain constant region genes to allow prodn. of the primatised antibodies have also been produced (see also AAW01817-19 and AAW01821-22). The primatised antibodies inhibit the B7:CD28 pathway, making them useful immunosuppressants for the treatment of autoimmune disorders and graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSLPAQLIGLLILCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDIFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                    Monkey monoclonal antibody binding human B7.1 or B7.2 antigen useful for treating autoimmune disease or graft-versus-host disease
                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1242; DB 18; Length 239; 100.0%; Pred. No. 1.8e-69; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaque primatized 7B6 light chain protein.
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                                                                                                               Claim 8; Fig 9A; 81pp; English.
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WPI; 1997-108638/10.
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                     N-PSDB; AAT62511
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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This sequence represents a primatized form of the antibody 7B6 light chain from macaque. This sequence is used in a method which studies new monoclonal antibodies (MAD's) that bind selectively to B7.1 (CD80) or to B7.2 (CD86) antipons and inhibits binding of these antigens to CD28. Such MaD's are specific immunosuppressants for treatment of diseases involving really seclinteractions, particularly autoimmune disease, specifically idopathic thrombocytopaenia purpura, systemic lupus srythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple solerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or their fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunosuppression, i.e. it inhibits antigen-specific immunosuppression and a surgion services.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein sequence of primatised form of the light chain of 7B6 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, macaque monkey; light chain; primatised antibody; 786 antibody; neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist; B7_1 antigen; CD86, B cell cancer; metastasis; tumour; B cell lymphoma; B cell letkaemia; autoimmune disease; graft-vs-host disease; immunosuppression; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSLPAQLLGLILLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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                                                                                  New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B cells, e.g. graft rejection or tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                           Example 7; Fig 4a; 87pp; English
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Best Local Similarity 100.0
Matches 239; Conservative
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Chimeric - Macaca sp.
1998-286601/25
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                       N-PSDB; AAV35486
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Gençore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

October 2, 2003, 09:07:34 ; Search time 10.503 Seconds Run on:

(without alignments)
2188.349 Million cell updates/sec

US-09-758-173-6 Perfect score:

1242 1 MSLPAQLLGLLLCVPGSSG.....EVTHQGLSSPVTKSFNRGEC 239 Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

pirl:*
pir2:* pir4:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2

ig Kappa chain NIG26 precursor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Dig #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C; Accession: DE0242 R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda Submitted to JTPID, November 1998 A; Description: Structure relationship of Kappatype light chains with AL amyloidosis: A; Reference number: JE0241

A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-315 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin hemology
F;16-91/Domain: immunoglobulin homology <IMM>

19 kappa chain V-J 19 kappa chain pre 19 kappa chain V r	Ig kappa chain Cr Ig kappa chain V r Ig kappa chain - h	Ig kappa chain pre Ig kappa chain V r Ig kappa chain - h Ig lambda-like cha	Ig kappa chain - h Ig kappa chain - h Ig kappa chain - h Ig kappa chain C r	Ig kappa chain pre anti-digoxin trans
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9 B B	8 8 8 8 4 8		4 4 4 4 0 1 2 8	44 50

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Ig kappa chain NIG2 precursor - human C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 15-198 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C; Accession: JE024# R; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H. Submitted to JIPID, November 1998 A; Description: A new subgroup of k type light chains (VkV) identified in cases of AL A; Accession: JE0244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 SGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTPP-TFGGGTKVEIKRTVAAPS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 VFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EVVWTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNRD 80
                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                                                                                                                                                                                       Score 915; DB 2; Length 215; Pred, No. 2e-55;
                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 1-215 <ALT-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                     17; Indels
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Best Local Similarity 80,9%
Matches 178; Conservative
RESULT 1
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A; Molecule type: protein A; Residues: 1-216 <ALI>
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C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
A; Eleoni, J; Ghiso, J; Goni, F; Frangione, B.
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogla A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
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A;Reference number: JE0243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain NIG93 precursor - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 C;Accession: JE0243 Fsequence_revision 05-Dec-1998 #text_change 21-Jan-2000 R;Allm, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; submitted to JIPID, November 1998
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EIVLTQSPGTLSLSPGERATLSCRASQSVSNN----YLAWYQQKPGQAPSLLIYDASSRA 56
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Query Match 73.1%; Score 908; DB 2; Length 215; Best Local Similarity 79.9%; Pred. No. 5.9e-55; Matches 175; Conservative 19; Mismatches 21; Indels
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A;Residues: 1-215 <ALI7
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;I6-90,Pomain: immunoglobulin homology <IMM>
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Rivan Engelen, F.; Schouten, A.; Molthoff, J.W.; Rooslen, J.; Dirkse, W.G.; Schots, A submitted to the EMBL Data Library, August 1994
A; Description: Coordinate expression of antibody subunit genes yields high levels of A; Reference number: $52028
A; Accession: $52028
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C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S$2028
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67.8%; Score 841.5; DB 2; Length 216;
Best Local Similarity 76.7%; Pred. No. 2e-50;
Matches 168; Conservative 21; Mismatches 27; Indels 3;
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F;16-92/Domain: immunoglobulin homology <IMM>
C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 78.4%
Matches 171; Conservative
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October 2, 2003, 08:56:23 ; Search time 6.59233 Seconds (without alignments) 1704.917 Million cell updates/sec
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1242
1 MSLPAQLIGILLICVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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SwissProt_41:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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SEQUENCE (BENCE-JONES PROTEIN AG).
MEDLINE-69234734; PubMed-4893682;
Titani K., Shinoda T., Putnam F.W.;
"The amino acid sequence of a kappa type Bence-Jones protein. 3. The complete sequence and the location of the disulfide bridges.";
J. Biol. Chem. 244:3550-3560(1969).
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Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
Immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
Ti). IV. The Complete amino acid sequence and its significance for
the mechanism of antibody production.;
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
                                           1 MSLPAQLLGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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MEDLINE-71064023; PubMed-5489770;
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"The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
       Gaps
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and J region
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Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
Steinmetz-Kayne M., Suter L., Watanabe S.,
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Grin Franch F., Shugar D. (eds.),
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"The covalent structure of a human gamma G-immunoglobulin. X.
Intrachain disulfide bonds.";
Biochemistry 9:3188-3196(1970).
       Indels
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Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr.,
"Cloned human and mouse kappa immunoglobulin constant
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[7]
       13;
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       Mismatches
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MEDLINE=68242259; PubMed=5586923;
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MEDLINE=71064027; Pubmed=4923144;
       13;
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        Conservative
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                 MEDLINE-70201507; PubMed=5447531; Xohler H., Shimizu A., Paul C., Putnam F.W.; Macroglobulin structure: variable sequence of light and heavy
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V -> L (IN INV(1,2) MARKER).

/FIG-VAR_003897.

D -> N (IN REF. 7 AND 8).

E -> Q (IN REF. 5 AND 6).
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Pred. No. 2e-37;
0; Mismatches 0; Indels
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PDB; 1HKL; 12-MAG-97.
PDB; 172; 08-AUG-01.
PDB; 1MIM; 15-MAY-97.
Genew; HGNC:5716; IGKC.
MIM; 147200; -
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO252, AAH2362.1;
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2.
SMART: SM00406; IGV; I.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                          C8WUK4

C95182

C86122

C951122

C951101

C95169

C95169

C901178

C901186

C901186

C901186

C901186

C901187

C901179

C901179

C901170

C901170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 101-MAR-2003 (TrEMBLrel. 23, 14) Pypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                     11
11
4
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                                                                                                    [1]
SEQUENCE FROM N.A.
TISSUE=Lung;
      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8TCD0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
    QBTCD0
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Q8nek0 homo sapien
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                                                                                                                                    2, 2003, 08:56:23; Search time 23.129 Seconds (without alignments) 2666.544 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                US-09-758-173-6
1242
1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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Q8VC16 mus m
Q8VC96 mus m
Q8VC90 mus m
Q9VC90 mus m
Q91VE mus m
Q91W12 mus m
Q91W18 mus m
Q91W18 Mus m
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                     GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                           830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
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Q8YCPO
Q8YCPO
Q91WF8
Q8YCBO
Q91WF8
Q91WS9
Q91WS9
Q9HUS9
Q9HLAS
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Q8NEK0
Q8NEK1
Q8VCI6
Q99M37
                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4: Sp_human:*
5: Sp_invertebrate:*
6: Sp_mammal:*
7: Sp_mhc:*
8: Sp_organelle:*
9: Sp_phage:*
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sp_rodent:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
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sp_bacteriap:*
sp_archeap:*
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2: sp_bacteria:*
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Match Length DB
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1103 1086 1086 864:5 843:5 808 808 1792 669:5 669:5 667:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 669:5 66

4207897654

Score

Result NO.

Gaps

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61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kba protein.
Hypothetical 26.2 kba protein.
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
                                                                                                                                                                                                                                                                                                                                                          Query Match 76.4%; Score 949.5; DB 4; Length 234; Best Local Similarity 77.8%; Pred. No. 4.3e-79; Matches 186; Conservative 24; Mismatches 24; Indels 5;
                                                      A Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
REMBL; BC0300813.13.13.15.
RICEPTO: IPR0037110; Ig-11ke.
R InterPro: IPR003306; Ig-c1.
R InterPro: IPR003306; Ig-MHC.
R InterPro: IPR003306; Ig-WHC.
R Pfam: PF00047; Ig-2.
R Pfam: PF00047; Ig-2.
R SMART; SM00406; IG-2.
R PROSITE; PS00296; IG-LIKE; 2.
R PROSITE; PS00299; IG-LIKE; 2.
R PROSITE; RS00290; IG-MHC; 1.
R HYPOCHAETICAL POTCHEIN.
SEQUENCE 234 AA; 25530 MW; 6316E8DEF8D132F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 69.6%; Score 864.5; DB 11; Length Best Local Similarity 68.2%; Pred. No. 2.8e-71; Matches 163; Conservative 30; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019760; AAH19760.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfom; PF00047; ig; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26224 MW; 35EC08E3DE5414AD CRC64;
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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238 AA; 2
[1]
SEQUENCE FROM N.A.
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Hypothetical
                                        TISSUE-Lung;
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                  PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
                                        61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YLQKPGQSPQLLIYLGSNRASGVPDRFSGSGSGTDFTLKISKVEAEDVGIYYCMQGLQTP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                              SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239
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                                                                                                                                                                                                                                                  QNNEXO:
QNNEXO:
QNNEXO:
QNOT-2002 (TEMBLE1 22, Created)
O1-OCT-2002 (TEMBLE1 23, Last sequence update)
O1-MAR-2003 (TEMBLE1 23, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Bukaryota, Metazoa, Ghordata, Craniata, Vertebrata, Euteleostomi;
Mammalia: Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNITY 1002 (TIEMBLEE). 22, Created)
01-0CT-2002 (TIEMBLEE). 22, Last sequence update)
01-MAR-2003 (TIEMBLEE). 23, Last annotation update)
Hypothetical protein.
Hymochetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tch 87.4%; Score 1085; DB 4; Length 2 al Similarity 87.9%; Pred. No. 1.3e-91; 210; Conservative 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC030814; ARH30814.1; -.
InterPro: IPR007110; Ig-11ke.
InterPro: IPR0073006; Ig-c1.
InterPro: IPR003596; Ig_v.
Ffam; PF00047; Ig; 2.
SMART; SM00407; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1. Hypothetical protein. SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;
                                                                                                                                                                                                                                        239 AA
                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                  121
                                                                                              181
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QBNEK1
                                                                                                                                                                                             RESULT 2
Q8NEK0
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Gaps

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DB 11; Length 238;

Appl Appl Appl Appl Appli Appli

Sequence Sequence S

Sequence Seq

Sequence S

ALIGNMENTS

Sequence Sequence

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ADDRIGONT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: 10 HUMAN 13 11 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: 10 HUMANGEUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSLPAQLIGLLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TESKIA, ROBIN L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 012712-131
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 1242; DB 3; Best Local Similarity 100.0%; Pred. No. 3.9e-101; Matches 239; Conservative 0; Mismatches 0;
US-09-027-449-56
US-08-804-444A-56
US-09-026-56
US-09-121-952A-56
US-09-214-340A-56
US-09-301-293-28
US-08-952-235-1
US-08-952-235-1
US-08-952-235-1
US-08-659-971-1
US-08-889-575-153
US-08-899-575-153
US-08-999-575-153
US-08-999-575-153
US-08-999-575-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08487550 Patent No. 6113898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 703-836-2021
| INPORMATION POR SEQ ID NO: 6
| SEQUENCE CHARACTERISTICS:
| LENGTH: 239 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| MOLECTLE TYPE: protein
| US-08-487-550-6
     GENERAL INFORMATION:
     RESULT 1
US-08-487-550-6
     8001084868888444444
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                                                                                                                                                                                                                                                                    US-09-758-173-6
1242
1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC 239
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-916-098A-56
US-08-398-613A-56
US-08-398-612A-56
US-08-398-612A-56
US-09-027-449-42
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US-09-027-449-42
US-09-027-449-62
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US-09-026-985-51
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
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Match 1
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Perfect score:
Sequence:
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Maximum DB
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0; Gaps

Length 239; Indels

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APPLICANT: BURKLY, LINDA C.
APPLICANT: THOMAS, DAVID W.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
APPLICANT: ROSA, JOSEPH J.
APPLICANT: ROSA, JOSEPH J.
APPLICANT: ROSA, JOSEPH J.
AITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 WYQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 PPTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 179
63 WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYXC-QQYYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSLPAQLLGLLLCVPGSSGEVVMTQSPLSLPITPGEPASISCRSSQSLKHS-NGDTFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; DB 2;
4.7e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: NORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: NO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION: 424
APPLICATION: WO. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION: 424
CLASSIFICATION: 424
APPLICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLIMOIS
COUNTRY: U.S.A.
COMMITTY: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 78.7%; Score 978; DB Best Local Similarity 80.4%; Pred. No. 4.7e Matches 193; Conservative 22; Mismatches
                                                                                                                                                                                                  US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1234
TELERA: 910/221-5314
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26,949
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NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETT
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BURKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-916-098A-56
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APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
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    YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTP 120
                                YQQKPGQPPRLLIYKVSNRDSGVPDRFSGSGAGTDFTLKISAVEAEDVGVYFCGQGTRTF 120
                                                                                             PTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                                                                                 SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09526098
Patent No. 6492134
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f: 699 Prince Street
Alexandria
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SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                           US-09-526-098-6
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2003, 09:18:44 ; Search time 89.7228 Seconds (without alignments) 421.442 Million cell updates/sec
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1242
1 MSLPAQLLGLLLCVPGSSG......EVTHQGLSSPVTKSFNRGEC
     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                       hits satisfying chosen parameters:
                                                                                                          587654 seqs, 158212981 residues
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Maximum Match 100%
Listing first 45 summaries
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Sequence 54, Appl Sequence 54, Appl Sequence 52, Appl Sequence 50, Appl Sequence 57, Appl Sequence 57, Appl Sequence 4, Appli

US-10-171-452A-44 US-10-171-452A-50 US-09-972-656-104 US-10-304-933-107 US-10-216-484-107 US-10-316-484-107 US-10-316-484-109 US-10-316-484-109 US-10-316-484-54 US-10-316-484-54 US-10-316-484-54 US-10-316-484-55 US-10-316-484-55 US-10-316-484-50 US-10-318-33-52 US-10-316-484-50 US-10-316-3382-11 US-09-249-0118-22 US-10-171-452A-39 US-10-171-452A-39 US-10-173-382-15 US-10-173-382-15 US-10-173-382-15 US-10-173-382-15 US-10-173-382-15

Sequence 1 Sequence 2 Sequence 3 Sequence 4 Sequence 4 Sequence 5

Sequence Sequence Sequence Sequence

Appl Appl

Sequence Sequence Sequence

US-10-171-452A-45 US-10-171-452A-51 US-10-384-933-129

Sequence 8, Appli

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Sequence 6, Application US/09948429B
Sequence 6, Application US/09948429B
Patent.No. US20020177689A1
GENERAL INFORMATION:
APPLICANT: Anderson Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS TITLE OF SEQUENCES: 12
CORRESPONDENCE: 12
ADDRESSEE: BURNES, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L:
REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703-836-6620
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US-09-948-429B-6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query Match

Score

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Result

1. / Cg02_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2. / Cg02_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
3. / Cg02_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4. / Cg02_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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14. / Cg02_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
15. / Cg02_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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15. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
16. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18. / Cg02_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

Published_Applications_AA:*

Database

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US-09-948-429B-6 US-10-114-807-6 US-10-291-532-6 US-10-124-905-6 US-09-992-600A-8 US-09-992-600A-8 US-09-992-570-8 US-10-154-678-8 US-10-1054-678-8 US-10-000-489-8 US-10-000-489-8 US-10-000-489-8 US-10-000-489-8 US-10-111-452A-38 US-10-111-452A-38 US-10-111-452A-38

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Sequence 6, Sequence (Sequence (

Description

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Conservative
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-807-6
                                                                                                   Best Local Similarity
Matches 239; Conser
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUAN B7.1 AND/OK B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: TO HUAN B7.1 AND/OK B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF,
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                             121 PIFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ 180
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                                                                                                                                                                                                                  Indels
                                                                                                                                                                            Query Match 100.0%; Score 1242; DB 10; Best Local Similarity 100.0%; Pred. No. 7.2e-78; Matches 239; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012712-131
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10124807
Publication No. US20030166207A1
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAWE: TESKIN, RObin L. REGISTRATION NUMBER: 35,030 REGISTRATION NUMBER: 012 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
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        703-836-2021
                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-948-4298-6
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MEDIUM TYPE: Floppy
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          TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/10291532
Publication No. US20030180290A1
GENERAL INFORMATION:
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HARIARRAN, KANDASAMY
APPLICANT: HANNA, NABIL
TITLE OF INVENTION: WEDIATED KILLING OF B CELL LYMPHOMA CELLS ALONE OR INTELE OF INVENTION: COMBINATION WITH OTHER THERAPIES
TITLE OF INVENTION: COMBINATION WITH OTHER THERAPIES
FILE REPEREBNEE: 037003291872
CURRENT PAPLICATION NUMBER: 08/2011-12
PRIOR PAPLICATION NUMBER: 08/10/291,532
CURRENT FILING DATE: 2001-11-09
PRIOR FILING DATE: 2001-11-09
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PAPLICATION NUMBER: 09/758,173
PRIOR PAPLICATION NUMBER: 09/758,16
PRIOR FILING DATE: 1999-08-26
PRIOR PLING DATE: 1999-08-26
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                  1 MSLPAQLEGILLLCVPGSSGEVVVTQSPLSLPITPGEPASISCRSSQSLKHSNGDTFLSW
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100.0%; Score 1242; DB 12;
Best Local Similarity 100.0%; Pred. No. 7.2e-78;
Matches 239; Conservative 0; Mismatches 0;
Score 1242; DB 12;
Pred. No. 7.2e-78;
Mismatches 0;
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AR108865 Sequence	AKZOSI99 Sequence BD063037 Identific	AK093806 Homo sapi	AX080951 Sequence	BCO1466/ HOMO Sapi	BC018747 Homo sapi	BC024289 Homo sapi	AYI72959 Homo sapi	A21385 Plasmid DNA	Y14737 Homo sapien	AKO97859 Homo sapi BC041037 Homo sapi	AK098817 Homo sapi	BD075127 Method fo	BC019046 Homo sapi	Y14735 Homo sapien	AKU9/36/ HOMO Sapı AF019036 Svn+hetic	sapi	AK097350 Homo sapi	AK097206 Homo sapi	AX594307 Sequence	AX616608 Sequence AX616908 Sequence	AX616611 Sequence	AX010615 Sequence	AV172957 Homo sapi	AK097366 Homo sapi	AX2//242 Sequence AK097360 Homo sapi	AK093636 Homo sapi	۲.	AX33330/ Sequence	M87789 Human (hybr	A29585 H.sapiens c RD078407 Aptigen-h	BD078408 Antigen-b AX556949 Sequence			DNA linear PAT 14-FEB-2001			Shestowsky,W.S. and Heard,C.	lbodies and tran
SUMMARIES	ID	AR108865	BD063037	AK093806	AX080951	BCO1456/	BC018747	BC024289	AY172959	A21385	HSIGGILH	AKU97859 BC041037	AK098817	BD075127	BC019046	HSIGGIKH	AKU9/36/ AF019036	AF027159	AK097350 AK097950	AK097206	AX594307	AX616608 AX616908	AX616611	AX010615	AX172957	AK097366	AX2//242 AK097360	AK093636	AX330501	AX33330/ AX334122	HUMIGHEPAH	A29585 BD078407	BD078408 AX556949	£		1437 bp nt US 6113898.	141		Hanna, N.	tized ans s -SEP-200
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FEATURES Location/Qualifiers 11437 Source		61 GIGCAACTGGAGICTGGGGGAGGCTTGGTCCAGCCTGGGGGTCCCTGAGAG 121 IGIGCAGTCTCTGGATTCACCTTCAGTGACCACACATGTTTGGTTCCGCCAGG 11	UB 181 GGGAAGGGCCGGAATGGGTAGGTTCATTAGAAACAAACCGAACGGTGGGACAACAGAA 240	TACATITCACATIGECGGGGGGGGGGGGAGGTACCTCGAATTCTGGGGCCAG	ACTAC 54 	Qy 661 TCCAGCAGCTTGGGCACCCAGACCTTGCAACGTGAATCACAAGCCCAGCAACACC 720 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	88 84 90 90 90 90

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October 2, 2003, 12:12:30 ; Search time 294.323 Seconds (without alignments) 13179.730 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description		Macaque primatized	DNA sequence of a	Primatised anti-hu	Bicistronic chimer	CDNA sequence #572	Anti-HIV-1 recombi	Human colon cancer	CDNA of the heavy
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ABX12855 AAS22593 AAS22593 AAQ20066 AAQ20066 AAQ206734 ABZ24633 AAV41421 AAV41429 AAS67284 AAQ49244 AAQ56655 AAQ56655 AAAG53219	ABX34965 AAS65516 ABX72100 AAQ26692 AAZ6699 AAZ6699 ABX31183 ABX65263 ABX63183 ABX65263 ABX63183 ABX65263 ABX635099 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951 AAX69951	in D in D in D in C, h in; in in;
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The Anderson DR, Brams P, Hanna N;

Anderson DR, Brams P, Hanna N;

MPI: 1998-286601/25.

BR P-PSDB; AAW63763.

WPT: 1999-286601/25.

BR P-PSDB; AAW63763.

WPT: 1999-286601/25.

Rew monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B proceeds.

PT inhibiting diseases that involve interactions between T and B proceeds.

PT and Brample 7: Fig 4b; 87pp; English.

Example 7: Fig 4b; 87pp; English.

Exa
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180 240 TACATTICACATIGICGGGGGGGGTGTCTGCTATGGAGGTTACTICGAATTCTGGGGCCAG 420 TACATTICACATIGICGGGGGGGTGTCTGCTATGGAGGTTACTICGAATTCTGGGGCCAG 420 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGGGGCCCTGGGCTGCCTGGTCAAGGACTAC 540 9 GGGAAGGGCCGGGATGGGTAGGTTCATTAGAAACAAACCGAACGCTGGGACAACAGAA ATGGGTTGGAGCCTCATCTTGCTCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG 1 ATGGGTTGGAGCCTCATCTTGCTCTTGTCGCTGTTGCTACGCGTGTCCAGTGTGAG GTGCAACTGGTGGAGTCTGGGGGGAGGCTTGGTCCAGCCTGGCGGGTCCCTGAGAGTCTCC 1GTGCAGTCTCTGGATTCACCTTCAGTGACCACTACATGTATTGGTTCCGCCAGGCTCCA TACGCCGCGTCTGTGAAAGACAGATTCACCATCTCCAGAGATTCCAAAAGCATCGCC TATCTGCAAATGAGCAGCCTGAAAATCGAGGACACGGCCGTCTATTACTGTACTACATCC GCGCCCTGGTCACCGTCTCAGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCA 100.0%; Score 1437; DB 19; Length 1437; llarity 100.0%; Pred. No. 1.1e-277; Conservative 0; Mismatches 0; Indels 0; Best Local Similarity Matches 1437; Conserv Query Match 61 121 121 181 241 301 301 361 361 121 121 481 셤 ò g Q g QQ g δ δ δ g Qγ $^{\circ}$ QΫ

1020 1080 1080 1200 AACTACAAGACGACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAG 1320 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT 1380 720 099 900 GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA 1437 CCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTAC 541 ITCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACC 601 INCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCC TCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC **AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACACGTGC** CCAGCACCACACACTCCTGGGGGGACCGTCACTCTTCCTCTTCCCCCCAAAACCCAAGGAC ACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAA GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACA GACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGACGGCGTGCATAATGCCAAGACA AAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTG CACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA 1021 CACCAGGACTGGGTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCA GCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGGAGAACCACAGGTATAC GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACCACAGGTAC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGGAGCAATGGGCAGCCGGAGAAC AAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAAC CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT of a primatised form of the heavy chain of 7B6 antibody AAS17245 standard; DNA; 1437 DNA sequence 12-MAR-2002 1141 1201 1381 481 601 661 661 721 781 781 901 961 1021 1081 1081 1201 1261 1261 1321 1321 1381 δ g g g 셤 ò ò ò g δ g ŏ Db ò g ò qq ò qq ò qq ò 음 á 셤 Q XEXDXXXX BX428863 602711488 AGENCOURT BX415920

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 Ewry cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7198.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
gol-bin/Cluster.cgi?seq-CSOD1009DE05NP1&cluster=7198.r. Contact :
Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InVitroGeh Corporation 1600
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BQ063185
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BX414495 BX414495
BQ062878 AGENCOURT
BX337477 BX337477
                                                                                                                                                                                                        2, 2003, 13:05:20 ; Search time 2376.47 Seconds (without alignments) 14696.420 Million cell updates/sec
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1437
1 AIGGGTTGGAGCCTCATCTT.......CCCTGTCTCCGGGTAAATGA 1437
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGCTGGCAGCAGGGGAACGTCT 1360
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/mol_type="mmm" saplens:
/db_xref="taxon.9606"
/clone="cSCoApOOITI13"
/tissue_type="#THYMUS"
/clone_lib="Homo saplens THYMUS"
/clone_lib="Ho
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               GCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGACGGCT
                                                                                                                                                                                                                                                                              226 CCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT
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BM 191 91006 EVRY cedex - Grant 
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
(bases 1 to 1142)
Li.M.B., Gruber,C., Jessee,J. and Polayes,D.
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Pred. No. 3.6e-205;
6; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1421 TGTCTCCGGGTAAATGA 1437
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Local Similarity 98.2%;
les 952; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Best Local S
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                                                                           /...zvg="mmno".homo sapiens"
/mol_type="mmno".homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PlaCENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PlaCENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pcWNSPORT 6 vector. Library was normalized."
88 a 296 c 396 g 267 t 54 others
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Avenue Genoscope sequence
Location/Qualifiers
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